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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 72512 Date: 10-19-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 101072111
Location (Bldg/Room#): 2D22 (Mailbox #): 2018 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: TD & cloning of RET16

Inventors (please provide full names): C. G. Todd et al.

Earliest Priority Date: 2/15/02

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID Nos 12 & 13

- Nucleotide data bases only
- please include Interference

12 na 1272 Search

13aa 384

- No size limits 6h-10/24/05

my

~~Signature~~

Thanks.

STAFF USE ONLY

Searcher: Jan

Searcher Phone #: 22504

Searcher Location: _____

Date Searcher Picked Up: 10/24/05

Date Completed: 10/25/05

Searcher Prep & Review Time: 10

Online Time: 415

Type of Search

☒ NA Sequence (#)

☐ AA Sequence (#)

☐ Structure (#)

☐ Bibliographic

☐ Litigation

☐ Fulltext

☐ Other

Vendors and cost where applicable

☐ STN ☐ Dialog

☐ Questel/Orbit ☐ Lexis/Nexis

☐ Westlaw ☐ WWW/Internet

☒ In-house sequence systems

☒ Commercial ☐ Oligomer ☐ Score/Length
☒ Interference ☐ SPDI ☒ Encode/Transl
☐ Other (specify)

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2005, 16:20:38 ; Search time 480 Seconds
(without alignments)
4735.793 million cell updates/sec

Title: US-10-077-111-13

Perfect score: 2047
Sequence: 1 MVKLITLADHGDVNCACF.....LTPNRLKALINRWLETHQK 384

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US10077111/runat_24102005_072845_8155/app.query.fasta.1.553
-DB=N-Geneseq_16Dec04 -QPM=faetap -SUFFX=ring -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosome2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NDB=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10077111.QCCH.1.1.352 -runat_24102005_072845_8155 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N-Geneseq_16Dec04.*

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3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
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8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047	100.0	1272	6	AAD45075 Human RET
2	1984	96.9	1553	6	AAD45071 Human RET
3	1984	96.9	1818	6	AAD45070 Human RET
4	1984	96.9	1996	5	ABV29028 Human pro
5	1984	96.9	1996	5	ABV23190 Human pro

6	1978	96.6	1773	8	AB224707 Human cel
7	1978	96.6	1811	10	ADB63535 Human CDN
8	1978	96.6	1817	10	ADB47507 Human CDN
9	1978	96.6	1844	4	AA158876 Human pol
10	1978	96.6	1844	5	ADQ99098 DNA encod
11	1978	96.6	1844	9	ADB48858 Novel hum
12	1958	95.7	1908	6	AAD45076 Human RET
13	1854	90.6	1623	4	AA164914 Beta-cren
14	1853.5	90.5	1826	5	AA160662 Human pol
15	1715.5	83.8	1686	5	ADM19385 Novel hum
16	1616.5	79.0	1901	6	AAD45073 Mouse RET
17	1226.5	59.9	1291	4	AA158364 Human GTP
18	1000	48.9	838	5	ADM19628 Novel hum
19	717.5	35.1	668	13	ADQ54461 Novel can
20	709	34.6	630	6	AAD45072 Human RET
21	627.5	30.7	446	5	ABV05038 Human pro
22	626.5	30.6	409	5	ABV14207 Human pro
23	621.5	30.4	441	5	ABV35301 Human pro
24	621.5	30.4	441	5	ABV44135 Human pro
25	597	29.2	366	4	AA136816 Probe #55
26	597	29.2	366	4	AAK30903 Human bon
27	597	29.2	366	4	AAK05311 Human bra
28	597	29.2	366	4	ABK30581 Human liv
29	597	29.2	366	6	ABK05651 Human gen
30	532	26.0	297	4	AA150015 Probe #18
31	532	26.0	297	4	AAK44005 Human bon
32	532	26.0	297	4	AAK18116 Human bra
33	532	26.0	297	4	ABK43659 Human liv
34	532	26.0	297	6	ABK18238 Human gen
35	509	24.9	419	3	AAH30188 Human col
36	352	17.2	520	6	AAD45074 Rat RET16
37	318	15.5	399	5	AAF66462 Novel hum
38	308.5	15.1	466	4	ABK58107 Human foe
39	308.5	15.1	466	4	AA137710 Probe #63
40	308.5	15.1	466	4	AAK31840 Human bon
41	308.5	15.1	466	4	AAK06182 Human bra
42	308.5	15.1	466	4	ABK31528 Human liv
43	308.5	15.1	466	6	ABK06599 Human gen
44	300	14.7	180	4	ABA70710 Human foe
45	300	14.7	180	4	AA150879 Probe #19

ALIGNMENTS

RESULT: 1	
AAD45075	standard; DNA; 1272 BP.
ID	AAD45075 standard; DNA; 1272 BP.
XX	
AC	AAD45075;
XX	
DT	27-DEC-2002 (first entry)
XX	
DE	Human RET16.2 splice variant DNA.
XX	
KW	Human; RET16; intracellular signal; inflammation-related disease; asthma;
KW	rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotection;
KW	transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KW	infectious respiratory disease; Crohn's disease; immunosuppressive; cancer;
KW	autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
KW	cellular migration disorder; cell proliferation disorder; calcification;
KW	hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
KW	cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KW	thalassaemia; vasotropic; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	111..1265
FT	/*tag= a
XX	/product= "Human RET16.2 splice variant protein"
PN	WO20026494-A2.

KM transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
 KM inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
 KM inacute respiratory distress syndrome; cardiast; ulcerative colitis;
 KM autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
 KM cellular migration disorder; cell proliferation disorder; calcification;
 KM hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
 KM cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
 KM thalassemia; vasotropic; open reading frame; ORF; gene; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 3..1541
 FT /*tag= a
 FT /product= "Human RET16 protein"
 FT /note= "CDS does not include start codon"
 FT /partial
 XX WO20026494-A2.
 XX
 XX PD 29-AUG-2002.
 XX PF 15-FEB-2002; 2002WO-US005162.
 XX PR 16-FEB-2001; 2001US-0269366P.
 XX PR 29-MAY-2001; 2001US-0294181P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX PI Todderud CG, Finger JN, Rillema J;
 XX DR P-PSDB; AAB28164.
 XX WPI: 2002-682760/73.
 PT New human, mouse or rat RET16 genes and proteins, involved in
 PT intracellular signaling cascade, useful for in gene therapy, particularly
 PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
 PT tumors or neoplasms.
 XX
 PS Claim 1; Page 150; 175pp; English.
 XX
 XX The invention relates to human, mouse or rat RET16 genes and proteins,
 CC involved in intracellular signaling cascade. The RET16 protein or
 CC polynucleotide is useful for treating an inflammation-related disease or
 CC disorder, e.g. rheumatoid arthritis; juvenile arthritis; psoriasis,
 CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
 CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
 CC bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
 CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
 CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
 CC disease or disorder also includes disorders associated with aberrant
 CC activation of the TNF-alpha pathway, disorders associated with aberrant
 CC cellular migration, proliferation, metastasis, juvenile idiopathic
 CC arthritis, haemogenous metastases of tumour cells, hyperinsulinaemia,
 CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
 CC tumour progression, Wegener's granulomatosis, stem cell transplantation
 CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
 CC injury, graft rejection, ischemic heart, coronary artery calcification
 CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
 CC sequence is human RET16 open reading frame (ORF) DNA
 XX
 SQ Sequence 1553 BP; 428 A; 327 C; 348 G; 450 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.86e-185 Length: 1553
 Score: 1984.00 Matches: 383
 Percent Similarity: 80.46% Conservative: 0
 Best Local Similarity: 80.46% Mismatches: 1
 Query Match: 96.92% Indels: 92
 DB: 6 Gaps: 1

US-10-077-111-13 (1-384) x AAD45071 (1-1553)

Qy 1 MetValIysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
 Db 111 ATGCTGAACCTGATTACACATTAGCTGATCAGGACAGATCTCACTGCTTGCCTTC 170
 Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
 Db 171 TCTTTTCCCTTCTGGCTACTCTCTCTTGACAAACAAATTCGCTGATCGTTAAGCT 220
 Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
 Db 231 GACTTTTACGAACTGCACATTCCTCCATTCGAACTTCATACCTATGCTGTCCTGTC 290
 Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyTyrThrValLeu 80
 Db 291 TGTTTCTCCCTTCAGGACATATTTTGGCATCTGTTTCAACACATGTTACCACTGCTTA 350
 Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
 Db 351 TGGAAATCTGAAATAAGACAGATGCTGCGAGTGGAGAACAGCCCTAGTGGCACCCCTGTG 410
 Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
 Db 411 AGGGTTTGCAGATTTTCCCACTCCACGTTGTGGCATCAGGGGCGAGCTGATGGAAGT 470
 Qy 121 ValValLeuThrPheAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
 Db 471 GTGGTTTGTGGAATGACACAGTCAATTAATATGATGCTGATGCTTAAAGATGCG 530
 Qy 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
 Db 531 TCCTTGGCGGCGATGTGATTTTCTCCATGAGAGCTTTCTTGCTACGTGCTCCTCATGT 590
 Qy 161 GlyAspLeuThrValTyrPheAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
 Db 591 GGGATTTTAAACAGTGGGAGTGAATAAATGAGGTGTCTGATGTGTGAAGACACATGAT 650
 Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnLeu 200
 Db 651 CTTGGATTTACCTGCTGCGCATTTTCTTCCACAGCCAGTTTCTGATGGAAACAAGGCTTT 710
 Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTyrIleValSer 220
 Db 711 CAGTTTCTTGCATCGGCATCATGGTGCAGATTTGCCAAATGCAAAATTTGATGTTCTT 770
 Qy 221 PheThrHisIleLeu----- 225
 Db 771 TTTAACCATATCTTAGGTTTGAATTAAATATTAAGTAACTGAGTGGGCACTGTGCT 830
 Qy 225 ----- 225
 Db 831 CCGTTCTGCGCTTGCTTTTCCCGATGGGCAAGTCTGATCTCAGGCTCAGTGAT 890
 Qy 225 ----- 225
 Db 891 AAGTGTCTCATAGTATATGATTAATACTGAGAATATTAATCTTACATGACTCAGCAC 950
 Qy 225 ----- 225
 Db 951 ACCAGTATGTCAAACTTGCTTTTGGACCTTAATACCTTTTACTTGTCTACTGTTC 1010
 Qy 226 -----AlaArg 228
 Db 1011 ATGACAAAACAGTGAACATCTGGCAATTTGACCTGGAAACACTTGGCCAAAGAGCGC 1070
 Qy 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTyrSerGluGluValLysThrTyr 248
 Db 1071 ACAAACATCAGCTGAAGCAATTTTACGAAGATTGGTCAAGAGAGATGCTCAACAATCG 1130
 Qy 249 LeuCysAlaIleAsnLeuLysAspLeuValGlyIlePheLysMetLeuAsnIleAspGly 268
 Db 1131 CTTTGTGCACAAATTTTAAAGATCTTGTGTGATTTTCAAGATGATTAACATTGATGGA 1190
 Qy 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288

Db 1191 AAGAACTGTGAATCTTACAAAGAAAGCTGGCATGATTTGAAAATGATCTCTA 1250
 QY 289 GYLeuAArgSerLeuValLeuAArgYllleGlulLeuAArgThryValYsSerLeu 308
 Db 1251 GGCTCTCGAGTAAATGTGCGAGAAATTTGAAGAGCTCGAGCAAGGTTAAATCCCTT 1310
 QY 309 SerSerGlyLeuProAArgPheIleCyPProIleThraArgLueuMetLysAspPro 328
 Db 1311 TCTTCAGGAATCTCTGATGAAATTTATATGTCCAACTAGAAACTTATGAAAGATCCG 1370
 QY 329 ValIleAlaSerAspGlyIleYsSerYrgLulYsGluAlaMetGluAsnTrpIleSerLys 348
 Db 1371 GTCATCGCATCAAGATGGCTATTTCATATGAAAAGAAAGCAATGAAATTGATCAGGAAA 1430
 QY 349 LysLysAArgThySerProMetThraAsnLeuValLeuProSerAlaValLeuThraProAsn 368
 Db 1431 AAGAAACGTAACAAGTCCCATGACAAATCTTGTCTTCACGCGGTACTTACACCAAAAT 1490
 QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
 Db 1491 AGGACTCTGAATAATGGCCATCATAGATGGCTGGAACACACCAAAAG 1538

RESULT 3
 AAD45070
 ID AAD45070 standard; DNA; 1818 BP.
 AC AAD45070;
 DT 27-DEC-2002 (first entry)
 DE Human RET16 DNA.
 XX
 XX Human; RET16: intracellular signal; inflammation-related disease; asthma;
 KM rheumatoid arthritis; psoriasis; multiple sclerosis; neuroproective;
 KM transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
 KM inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
 KM inactive respiratory distress syndrome; cardiac; ulcerative colitis;
 KM autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasia;
 KM cellular migration disorder; cell proliferation disorder; calcification;
 KM hyperinflammation; diabetes type 2; systemic lupus erythematosus; tumour;
 KM cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
 KM thalassemia; vasotropic; gene; ds.
 KM
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS /tag= a
 FT /product= "Human RET16 protein"
 PN MO200266494-A2.
 XX
 PD 29-AUG-2002.
 XX
 PP 15-FEB-2002; 2002MO-US005162.
 XX
 PR 16-FEB-2001; 2001US-0269366P.
 PR 29-MAY-2001; 2001US-0294181P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 DR Todderud CG, Finger JN, Rillema J;
 DR MPI, 2002-682760/73.
 DR P-PSDB; AAB28163.
 XX
 PT New human, mouse or rat RET16 genes and proteins, involved in
 PT intracellular signaling cascade, useful for in gene therapy, particularly
 PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
 PT tumors or neoplasms.
 XX
 PS Claim 1; Page 147-148; 175pp; English.

XX
 CC The invention relates to human, mouse or rat RET16 genes and proteins,
 CC involved in intracellular signaling cascade. The RET16 protein or
 CC polynucleotide is useful for treating an inflammation-related disease or
 CC disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
 CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
 CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
 CC bowel disease, Crohn's disease, ulcerative colitis, inactive respiratory
 CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
 CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
 CC disease or disorder also includes disorders associated with aberrant
 CC activation of the TNF-alpha pathway, disorders associated with aberrant
 CC cellular migration, proliferation, metastasis, juvenile idiopathic
 CC arthritis, haematogenous metastases of tumour cells, hyperinflammation,
 CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
 CC tumour progression, Wegener's granulomatosis, stem cell transplantation
 CC complications, ischaemia-reperfusion injury, thalassemia, acute lung
 CC injury, graft rejection, ischaemic heart, coronary artery calcification
 CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
 CC sequence is human RET16 DNA
 XX

SO Sequence 1818 BP; 523 A; 373 C; 382 G; 540 T; 0 U; 0 Other.

Alignment Scores:
 Pred. No.: 3,58e-185 Length: 1818
 Score: 1984.00 Matches: 383
 Percent Similarity: 80.46% Conservative: 0
 Best Local Similarity: 80.46% Mismatches: 1
 Query Match: 96.92% Indels: 92
 DB: 6 Gaps: 1

US-10-077-111-13 (1-384) x AAD45070 (1-1818)

QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnProGlyAlaPhe 20
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 QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuYsSerLeuArg 40
 Db 208 TCTTTTCCCTCTTGCTGCTACTGCTCTTGACAAACAATTCGCTGATCTGTTACGT 267
 QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraAlaValHisCysCys 60
 Db 268 GACTTTACTGAACCTGGCCATCTTCATGGAAGTTCCATACCTGATGCTCCACTCTGC 327
 QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
 Db 328 TGTTCCTCCCTTCAGAGACATATTTGGCATGCTGTCAACAGATGTACCACTGTCTTA 387
 QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
 Db 388 TGGAAATACGAAATATGACAGATGCTGGCAGTGAATGGAACAGCTGATGCGACCTGTG 447
 QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
 Db 448 AGGGTTTGGCAGATTTTCCCAAGCTCCACGTTGGTCATCGGGGCCACTGATGMACT 507
 QY 121 ValValLeuThrAsnAlaGlnSerTyrlYsLeuTyraArgCysGlySerValLysAspGly 140
 Db 508 GTGGTTTGTGGATGACAGATCATACAAATTAATATGATGATGTATTAAGATGGC 567
 QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
 Db 568 TCTTGGCGGCAATGTCATTTCTCTTAATGGAAGCTTTTGTGCTGCTGCTCTGATGT 627
 QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
 Db 628 GGGATTTTAACAGTGGCATGATGATAAATGAGGTGCTCATATGATGAATAAGACATGAT 687
 QY 181 LeuGlyIleThrCysGlyAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
 Db 688 CTTGGAATTAACCTGCTGCAATTTTCTTCAACAGCCAGTTTGTGATGAGAACAGGTCTTT 747

QY 201 GlnPhePheargheulaseCysGlyGlnAspCysGlnValIleThrIleValSer 220
DB 748 CAGTTTTCGATCGCATGTGGTCAGAGATTGCCAAATTCGATTTGCTTCT 807
QY 221 PheThrHisIleLeu----- 225
DB 808 TTTACCAATATCTTAGTGTGTAATTAATAAAGTACACTGAGTGGCAGCTGTCT 867
QY 225 ----- 225
DB 868 CTTGTTCTGGCTTGTCTTTTCCCATGATGAGGAGATGCTAGTCCAGGGTCAGTGAT 927
QY 225 ----- 225
DB 928 AACTGTCTCATAGTATATGATTAATACTGAGAAATTACTTCACACATGACTCAGCAC 987
QY 225 ----- 225
DB 988 ACCAGTATGTCAACAATTGTGCTTTGACACTAATACCTTTTACTTGTGCTAGTTCA 1047
QY 226 -----AlaArgArg 228
DB 1048 ATGACAAACACTGAAACATCTGGCAATTGACCTGGAAACACTTTCACAAAGAGCGC 1107
QY 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTrp 248
DB 1108 ACGAAACATAGCTGAGCAATTTACCGAAGATTGGTCAAGGAGATGCTCAACATGG 1167
QY 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
DB 1168 CTTTGTGACACAGATTTAAAGATCTTGTGTATTTTCAAGATGATTAACATGATGAGA 1227
QY 269 LysGluLeuLeuLeuLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
DB 1228 AAGAACTGTGATCTTACAAAGAAAGTCTGCTCATATTTGAAATTTGAATCTCTA 1287
QY 289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
DB 1288 GGACTGCTGTAAGTGAAGTCTGAGGAAATTTGAGAGCTCAGACCAAGTTAAATCCCTT 1347
QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
DB 1348 TCTTCAGAGATTCCTGATGATTTATATGTCCAATACTAGAGAACTTATGAAAGATCCG 1407
QY 329 ValIleAlaSerAspGlyIleLysSerThrGluLysGluAlaMetGluAsnThrIleSerLys 348
DB 1408 GTCATGCAATCAAGATGGCTATTCATATGAAAGAGAACCAATGGAAATTTGATCAGCAA 1467
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1468 AAGAAACGTACAGTCCCATGACAAATCTGTTCTTCTCAGCGGATTTACACCAAT 1527
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
DB 1528 AGGACTCTGAATAATGGCCATCAATAGATGGCTGAGACACACCAAAAG 1575
RESULT 4
ABV29028 standard; cDNA; 1996 BP.
ID ABV29028
AC ABV29028;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 29019.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX MO200160860-A2.
XX

PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001MO-US005171.
XX
XX 17-FEB-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE.
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1, Page 6145-6146; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other;
XX
XX Alignment Scores:
Pred. No.: 4.09e-185 Length: 1996
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: Gaps: 1
US-10-077-111-13 (1-384) x ABV29028 (1-1996)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
DB 16 ATGGTGAAACTGATTCACACATTAGCTGATCAATGACATGTCAACTGCTGCTTC 75
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuIleArgSerLeuArg 40
DB 76 TCCCTTTCCCTCTGTGCTACTTCTGCTCTCTGACAAACAATTCGCTGATCTGTTACGT 135
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrIleValIleHisCysCys 60
DB 136 GACTTTACTAATCACTGCACATTCCTCAATGAAGTTCAATCACTATGCTGCTCACTGCTC 195
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 196 TGTTTCTCCCTTCAGGACATATTTTGGCATCGTGTTCACACAGATGTATCCACGTCTTA 255
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
DB 256 TGGAAATCTGAAATAGACAGATGCTGAGTATGAGAAACAGCTAGTGCCAGCCCTGTG 315
QY 101 ArgValCysGlnInPheSerProAspSerThrCysLeuAlaSerGlyAlaIleAspGlyThr 120
DB 316 AGGGTTTGGCAGATTTTCCCACTCCACGCTGTTTGGCATCAGGGGAGCTGATGAGACT 375
QY 121 ValValLeuThrAsnAlaGlnSerIleLysLeuIleValArgCysGlySerValLysAspGly 140

```
Db 376 GTGGTTTGTGGATGCACAGTCATCAAAATTATATAGATGTGTGTTAAAGATGGC 435
Qy 141 SerLeuAlaAlaCysAlaPheSerProAnGlySerPhePheValThrGlySerSerCys 160
Db 436 TCCCTGGCGGCGATGTCATTTCTCTTAATGGAAGCTTCTTGTCTCACTGGCTCCTCATG 495
Qy 161 GlyAspLeuThrValTyrPheAspLysMetArgCysLeuHisSerGlnLysAlaHisAsp 180
Db 496 GGTGATTTTAACACTGTGGAGTGAATAAATGAGGTGCTGTGATGTAAGAAAAGCAATGAT 555
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
Db 556 CTGGGAATTACCTGCTGCATTTTCTTCTCAAGACCACTTCTGATGAGAAACAAGTCTT 615
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIleTyrPheLeuValSer 220
Db 616 CAGTTTTCGACTGGCATCATGTGGTCAGAGATTGGCCAATGCAAAATTGGATTGTTTCT 675
Qy 221 PheThrHisIleLeu----- 225
Db 676 TTTTACCATATCTTTAGCTTTTGAATTAATAATAAAAGTACACTGAGTGGCCTGCTCT 735
Qy 225 ----- 225
Db 736 CCGTTCTGGCTTGCTGCTTTTCCCATGATGGCAGATGTCTCAGGGTCAGTGAAT 795
Qy 225 ----- 225
Db 796 AAGTCTGTATAGTATATGATACTAATACTAGAGATAATACCTTGCACATTGACTCAGAC 855
Qy 225 ----- 225
Db 856 ACCAGGTATGTCACAACCTTGTCTTTGGACCTTAATACCTTTTACTTGTACTGCTTCA 915
Qy 226 -----AlaArg 228
Db 916 ATGACAAAACAGTGAACATCTGCAATTGACCTGGAAACACTTTGCCAAGCAAGCGCG 975
Qy 229 ThrGlnHisGlnLeuLysGlnPheThrGlnAspTyrSerGlnGlnValIleSerThrTrp 248
Db 976 ACAGAACAATCAGCTGAAGCAATTTACCGAAGATTGGTCAGAGAGAGATGTCCTCAACATGG 1035
Qy 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db 1036 CTTTGGCACAAGATTTTAAAGATCTTGTGATTTTCAAGTGAATAACATTGATGCA 1095
Qy 269 LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu 288
Db 1096 AAGAAGCTGTTGAATCTTACAAAAGAAAGCTGGCTGATGATTTGAAAATTGAATCTCTA 1155
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
Db 1156 GGACTGCTGAGTAAAGTGTGAGGAAATTTGAAGAGCTCGAGCAAGGTTAAATCCCTT 1215
Qy 309 SerSerGlyIleProAspGlnPheIleCysProIleThrArgLysLeuMetLysAspPro 328
Db 1216 TCTTCAGAAATTCCTATGATTAATATATGTCCTCAATTAAGAACTTAAGAAAGATCCG 1275
Qy 329 ValIleAlaSerAspGlyTyrSerTyrGlnLysGlnAlaMetGlnLysAntPrlSerLys 348
Db 1276 GTCATCGCATCAATGCTATTCATATGAAAAGAAAGCAATGAAAATTGATCACAACAA 1335
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1336 AAGAAACGTAACAAGTCCCATGACGAACAAATCTTCTTCCTTCACGGGATCTTACACCAAA 1395
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTyrLeuGlnThrHisGlnLys 384
Db 1396 AGGACTCTGAAAATGGCCATCATAGATGCGTGGAGACACACCAAAAG 1443
```

RESULT 5
ABV23190

```
ID ABV23190 standard; cDNA; 1996 BP.
XX
AC ABV23190;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23181.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; 86.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
XX
PD 23-ANG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-018319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 4166-4167; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (i) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement; (i) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other;
XX
Alignment Scores:
Pred. No.: 4,09e-185 Length: 1996
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Beer Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 5 Gaps: 1
US-10-077-111-13 (1-384) x ABV23190 (1-1996)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValLysCysCysAlaPro 20
Db 16 ATGGTGAAACGTAGTTTCAACATTAAGCTGATGATGAGAGAGTCAATGCTGTGCTTCT 74
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
Db 76 TCCCTTTTCCCTCTTGGCTACTGCTGCTTGGACAAACAAATTCGCTGATCGTTACGT 135
Qy 41 AspPheThrGlnLeuProHisSerProLysLysPheHisThrTyrAlaValHisCysCys 60
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XX Claim 5: Page 235-236; 238bp; English.

CC The present sequence is that of Incyte clone 7483131CBI encoding human
CC CGDP-19, a novel protein associated with cell growth, differentiation and
CC death. A representative cDNA library for the polynucleotide is KIDNOT19
CC derived from kidney tissue. Structural features establish the encoded
CC protein as being associated with cell growth, differentiation and death,
CC and as showing sequence and structural similarity to human apoptotic
CC protease activating factor 1. The invention is based on novel human CGDP-
CC 1 to -221 proteins (see ABP58330-50), the polynucleotides encoding them
CC (see AB24689-709), and to the use of these for the diagnosis, treatment
CC or prevention of cell proliferative disorders including cancer,
CC developmental disorders, neurological disorders, autoimmune disorders,
CC reproductive disorders, and disorders of the placenta, and in the
CC assessment of the effects of exogenous compounds on the activity and
CC expression of proteins and nucleic acids associated with cell growth,
CC differentiation and death. CGDP polynucleotides are also used in a
CC claimed microarray and in a claimed method of generating an expression
CC profile of a sample

XX Sequence 1773 BP; 535 A; 334 C; 371 G; 533 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.35e-184 Length: 1773
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 8 Gaps: 1

US-10-077-111-13 (1-384) x AB224707 (1-1773)

QY 1 MetValLysLeuIleHieThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
DB 60 ATGTGAACTGATTTCACACATTAGCTGATGATGGTACAGATGTCACCTGTCCTTC 119
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuIleYrSerLeuArg 40
DB 120 TCTTTTCCCTCTGGTACTTCTCTCTGACAAACAAATTCGCTGATCGTTAAGT 179
QY 41 AspPheThrGluLeuPheHisSerProLeuLysPheHisThrTyralaValHisCysCys 60
DB 180 GACTTAACTGAACTGCACATCTCTCCATGAACTTCACTATGCTGTCCTCCTGTCG 239
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 240 TGTTTCTCCCTCAGACATATTTTGGCATCGTTCACACAGTGGTACCACCTGCTTA 239
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
DB 300 TGGAACTACTGAAATGACAGATGCTGCGATGGTGAACAGCCTAGTGGCAGCCCTGTG 359
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
DB 360 AGGAGTTTGCAGATTTTCCAGACTCCACGCTGTTTGGCACTCAGGGGACGCTGATGAAC 419
QY 121 ValValLeuTrpAsnAlaGlnSerTyrlsLeuTyArgCysGlySerValLysAspGly 140
DB 420 GTGCTTTTGGGATGACAGCTCATACAAATTATATGATGTGTTAAAGATGGC 479
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
DB 480 TCCTTGGCGGAGTGTGATTTTCTCTTAATGGAAGCTTTCTTTGCACTGGCTCCTCATGT 539
QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCysAlaLeuHisSerGlyLysAlaHisAsp 180
DB 540 GGGGATTTTAAACAGTGGGATGATAAAAATAGGCTGTGATGTGAAAAAGACACATGAT 599
QY 181 LeuGlyIleThrCysAspAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
DB 600 CTTGGAATTAACCTGCTGCGATTTTCTTTCACAGCCAGTTCTGATGGAGAACAGGCTCT 659

QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrIleValSer 220
DB 660 CAGTTTTCGACTGGCATCATGTGGTCAAGATTGCCAGATTCGCAAAATTTGGATTTGTTCT 719
QY 221 PheThrHisIleLeu----- 225
DB 720 TTATCCCATATCTTTAGTCTTTTGAATTAAATATATAAGTACACTGAGTGGCATGTGCT 779
QY 225 ----- 225
DB 780 CCTGTTCTGGCTTGTCTTTTCCCATGATGGGACAGATCTGATCTCAGGCTCAGTGCAT 839
QY 225 ----- 225
DB 840 AAGTCTCATATGATATATGATACTAATACAGAAATATATCTTCACACATTGACTGACAC 899
QY 225 ----- 225
DB 900 ACCAGGATATGTCACACTTGTGCTTTTGGACCTTAATACCTTTTACTTGTCTACGTGTC 959
QY 226 -----AlaArgArg 228
DB 960 ATGGACAAAACAGTGAACATCTGGCAATTGACCTGGAACACTTGGCCAGCGAGAC 1019
QY 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValSerThrTrp 248
DB 1020 ACAGAACATCAGCTGGAAGCAATTTCCGAAGATTGGTTCAGAGAGAGATCTTCACATCG 1079
QY 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePhePheMetCysHisGlnIleAspGly 268
DB 1080 CTTTGTGACACAAAGATTAAAGATCTTGTGATTTTCAAGATGATTAACATTTGATGGA 1139
QY 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
DB 1140 AAAGAACTGTGAATCTTACAAAGAAAGTCTGCTGATGATTTGAAATTTGAATCTCTTA 1199
QY 289 GlyLeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeu 308
DB 1200 GAGCTCGTAGTAAAGTGTGAGGAAATTTGAAGAGCTCAGGACCAAGCTTAATTCCTTT 1259
QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluCysLysAspPro 328
DB 1260 TCTTCAGGAATTCCTGATGATTAATTTATGTCTCAATTAACAGAACTTTGAAAGATCCG 1319
QY 329 ValIleAlaSerAspGlyTyrlsSerTyrlsGluLysGluAlaMetGluLysAsnTrpLysSerLys 348
DB 1320 GTCATGCGATCAGATGCTATTCATATGAAAGAAAGACATGAAATTTGATCAGACAAA 1379
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1380 AAGAAACGTAAACAGTCCCATGACAAATCTTGTCTTCTTCAGCGGTACTTACACCAAA 1439
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
DB 1440 AGGACTCTGAAATATGGCCATCAATATGATGCTGGAGACACACCAAAAG 1487
RESULT 7
ID ADB63535 standard; cDNA; 1811 BP.
XX ADB63535;
AC ADB63535;
DT 04-DEC-2003 (Firev entry)
XX
DE Human cDNA encoding clone TEST120264530.
XX
XX Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
XX tissue regeneration; cell regeneration; membrane protein;
XX signal transduction-related protein; transcription-related protein;
XX osteoporosis; neurological disease; cancer; tumour.
OS Homo sapiens.
XX

FT	Key	Location/Qualifiers
FT	CDS	150..1580
FT		/tag= a
FT		/product= "Clone TEST120264530 protein"
XX		
PN	EP1308459-A2.	
XX		
PD	07-MAY-2003.	
XX		
PE	28-MAR-2002; 2002EP-00007401.	
XX		
PR	05-NOV-2001; 2001JP-00379298.	
PR	25-JAN-2002; 2002US-00350978.	
XX		
PA	(HELI-) HELIX RES INST.	
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
PI	Isoaga T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,	
PI	Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,	
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y,	
XX		
DR	WPI: 2003-450961/43.	
XX	P-PSDB; ADB65505.	
PT	New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.	
PT		
PS	Claim 1; Page; 222pp; English.	
XX		
CC	The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotides or its partial peptide, an antibody binding to the polypeptide or peptidated peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between them, a transformant carrying the polynucleotide in an expressible manner, and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesizing the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours). The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The CC sequence presented is a CDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but CC is based on sequence information supplied by the European Patent Office.	
XX		
SO	Sequence 1811 BP; 520 A; 352 C; 399 G; 540 T; 0 U; 0 Other;	
XX		
Al	Alignment Scores:	
Pred. No.:	1,39e-184	Length: 1811
Score:	1978.00	Matches: 382
Percent Similarity:	80.25%	Conservative: 0
Best Local Similarity:	80.25%	Mismatches: 2
Query Match:	96.63%	Indels: 92
DB:	10	Gaps: 1
US-10-077-111-13 (1-384) x ADB65335 (1-1811)		
OY	1 MetValysIeuIlleHisThrIleuAlaAspHisGlyAspAspValAsnCysCysAlaPhe	20
Dd	150 ATGGTGAACCTGATTCACACATTAGCTGATCATGTGAGTGACGATGCACTGCGCTTC	209
OY	21 SerPheSerLeuLeuAlaThrCysSerLeuAspArgTrpIleArgLeuTyrSerLeuArg	40
Dd	210 TCCTTTCCCTCTTGCTACTGCCTCTCTTGACAAACATTCCGCTGACTGTTACGT	269

OY	41	AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys	60
Db	270	GACTTTACTGACGCCACATTCCTCCATTGAAAGTTTATACCTAAGCTGTCCACTGCTGC	329
OY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	330	TGTTTCTCCCTTCAGGACATATTTTGGCATCGTGTTCAACAGATGGTACCACTGTCTTA	389
OY	81	TrpAsnThrGluLeuGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
Db	390	TGGAAATCTGMAAATGACACAGATGCTGGCAGTGTGGAACACGCTTATGGCACGCCCTGTG	449
OY	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr	120
Db	450	AGGGTTTGGCCAGTTTTCCTCCAGACTCCACGCTGTTTGGCATTCAGGGCCACTGATGGAATC	509
OY	121	ValValLeuTrpAsnAlaGlnSerTyrLysLeuThrArgCysGlySerValLysAspGly	140
Db	510	GTGCTTTTGTGGATGACACAGTCTATCAAAATTATATGATGTGGTACTGTTAAAGATGAC	569
OY	141	SerLeuAlaAlaCysAlaPheSerProAspGlySerPhePheValThrGlySerSerCys	160
Db	570	TCTCTGGCGGAGTGTGCATTTCTCCAAAGAAAGCTTTCTTGCACTGGCTCTCAATGT	629
OY	161	GlyAspLeuThrValITrPAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp	180
Db	630	GGTATTTTAAACAGTGTGGATGATAAATAGAGTGCTGCATATGTAATAAAGCACATGAT	689
OY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu	200
Db	690	CTTGGAAATTAACCTGCTCGAATTTTCTTCACAGCAAGTTTCTGATGGAAACAAGTCTT	749
OY	201	GlnPhePheArgLeuAlaSerCysGlyGlyAspCysGlnValLysIleThrPileValSer	220
Db	750	CAGTTTCTTGGACTGGGCATCATGTGGTCAAGGATGGCCAAATTTGGATTGTTCT	809
OY	221	PheThrHisIleLeu-----	225
Db	810	TTTATCCCATATCTTAGCTTTGAATTAATAATATTAAGTACACTGAGTGGGCACTGTGCT	869
OY	225	-----	225
Db	870	CTGTCTTGCGCTTGCTGCTTTTCCCATGATGGCAGATGCTGACTGACGGGTACGTGAT	929
OY	225	-----	225
Db	930	AAAGTCTGCATAGTATATGATATACTAATACAGAGATATATCTTCACATTTGACTCAAGCAC	989
OY	225	-----	225
Db	990	ACCAGTATGTCAACACCTGTGCTTTTGGCACTAATACCTTTTACTTGTACTGTCTTA	1049
OY	226	-----AlaArg	228
Db	1050	ATGACACAAAACAGTGAACATCTGSCAATTTGACTGGAACACTTTGGCCACAGCAGAC	1109
OY	229	ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTyr	248
Db	1110	ACAAACAATCAGCTGAGACGAATTTTACCGAAGATTTGTCAAGAGAGATGTCTCAACATGG	1169
OY	249	LeuGlyValIleGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly	268
Db	1170	CTTTGTGACACAGATTTTAAAGATCTGTGTGGTATTTTTCAAAGATTAACATTGATGGA	1229
OY	269	LysGluLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu	288
Db	1230	AAAGACATGTTGATCTTACAAAAGAAAGTCTGGCTGATGATTTGAAATTTGATATCTTA	1289
OY	289	GlyLeuLysSerLysValIleuArgLysIleGluGluLeuArgThrLysValLysSerLeu	308
Db	1290	GGACTCGGTAGTAAAGTGTGAGGAAAAATTGAACAGCTCAGACCAAGGATTAAATCCCTT	1349

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QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
DB 1350 TCTTCAGGAATTCCTGATGTAATTTATATGTCACATATCACTAGAGAACTTATGAAAGATCCG 1409
QY 329 ValIleAlaSerAspGlyIleTyrSerIleGluLysGluAlaMetGluMetTrpIleSerLys 348
DB 1410 GTCATGGCAATCAATGCTATTCATATGAAAGAACCAATGAAATTTGATCAGCAAA 1469
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1470 AAGAAACGTACAAGTCCCATGACAAATCTTCTTCTTCAGCGGACTTACACCAAAAT 1529
QY 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
DB 1530 AGGACCTGAAATAATGGCCATCAATAGATGGCTGGAGACACACCAAAAG 1577

RESULT 8
ADB47507
ID ADB47507 standard; cDNA; 1817 BP.
XX
AC ADB47507;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA upregulated in dendritic cells SEQ ID NO 207.
XX
KM aa; gene; human; dendritic cells; high throughput; cancer;
KM infectious disease; autoimmune disease; allergy;
KM graft versus host disease; vaccine enhancing; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003134283-A1.
XX
PD 17-JUL-2003.
XX
PF 03-OCT-2001; 2001US-00971392.
XX
PR 03-OCT-2000; 2000US-0237652P.
XX
PA (PETE/) PETERSON D P.
PA (PEAR/) PEARSON C I.
PA (COCK/) COCKS B G.
XX
PI Peterson DP, Pearson CI, Cocks BG;
XX
DR WPI; 2003-662509/62.
XX
PT New combination comprises cDNAs that are differentially expressed in
PT dendritic cells useful for preparing a composition for diagnosing or
PT treating cancer, infectious disease, autoimmunity, allergy or graft
PT versus host disease.
XX
PS Claim 1; SEQ ID NO 207; 28bp; English.
XX
XX The invention relates to a combination comprising cDNAs that are
CC differentially expressed in dendritic cells (DC). Also included is a high
CC throughput method for detecting differential expression of one or more
CC cDNAs in a sample containing nucleic acids. The combination is useful for
CC preparing a composition for diagnosing, treating and monitoring the
CC treatment of cancer, infectious disease, autoimmunity, allergy or graft
CC versus host disease, or for enhancing a vaccine. The present sequence
CC represents a human cDNA upregulated in dendritic cells. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=20030134283.
XX
SQ Sequence 1817 BP; 519 A; 373 C; 383 G; 542 T; 0 U; 0 Other;
XX
```

```
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 10 Gaps: 1
US-10-077-111-13 (1-384) x ADB47507 (1-1817)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
DB 148 ATGGTAAACTGATTCACACATTAGCTGATTCATGGGACGATGTCAACTGCTGCTTC 207
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleGArgLeuTyrSerLeuArg 40
DB 208 TCCCTTTCCCTCTTGGCTACTGCTCTCTTGGACAAACAAATTCGCTGACTCGTTACGT 267
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheIleThrTyrAlaValHisCysCys 60
DB 268 GACTTTACTGAACTGGCCACATTTCTCCATTGAACTTTTCATACCTATGCTGCTGCTG 327
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeu 80
DB 328 TGTTCCTCCCTTCAGACATATTTTGGCATCGTGTCAACAGATGTAACACTGCTGCTA 387
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
DB 388 TGGAAATACAGAAATAGACAGATGCTGGAGATGGAACAGCTTATGGAGCCCTGTG 447
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
DB 448 AGGCTTTGCCAGTTTCCCAAGCTCCACAGCTCAGCTGTTGGCATCAGGGCAGCTGATGA 507
QY 121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
DB 508 GTGGTTTGGGAATGACAGATCATCAATAATATATAGATGGTGTATTAAGATGGC 567
QY 141 SerLeuAlaAlaLysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
DB 568 TCCCTGGCGGACAGTGCATTTCTCTTAATGGAAGCTTCTTGTGCATGCTGCTCTCA 627
QY 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyIleValAlaHisAsp 180
DB 628 GGTGATTTTAACTGTCGATGCGGATGATTAATAAGAGTGTCTGCAATGTAATAAGCACTG 687
QY 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
DB 688 CTGGAAATTACCTGCTGCATTTTCTTCACAGCCAGTTTCGATGAGACAACAGGCTCTT 747
QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValIleTrpIleValIleSer 220
DB 748 CAGTTTTTTCGACTGGCATCATGTGTGTCAGATTGGCAAAATTTGATTTGTTCT 807
QY 221 PheThrHisIleLeu----- 225
DB 808 TTTTACCCATATCTTTAGGTTTGAATTAATAATATAAAGTACACTGAGTGGCATGTGCT 867
QY 225 ----- 225
DB 868 CTGTTCGTGGCTGTGCTTTTCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 927
QY 225 ----- 225
DB 928 AAGTCTGTCACTAGTATATGATACTAATACTGACAAATATCTTCACACATTGACTCAGCAC 967
QY 225 ----- 225
DB 988 ACCAGGATGTCACAACTGTGTGCTTTTGACACTTAATACCTTTTACTGTGTTACTGTTCA 1047
QY 226 -----AlaArgArg 228
DB 1048 ATGACAAAACAGTGAACATCTGGCAATTTGACCTGGAAAACACTTTGCCAAGCAAGAGAGC 1107
QY 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTrp 248
DB 1108 ACAGAACATCAGCTGAAGCAATTTACCGAAGATTGTCAGAGGAGATGTCATCAACATGG 1167
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QY 201 GlnPhePheArgLeuValAspCysGlyGlnAspCysGlnValIleTyrIleValSer 220
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  |||
Db 764 CAGTTTTCGACTGGCATCATGGTGCAGAGATTGCCAAATTCGAATTTGATTTGTTCT 823
QY 221 PheThrHisIleLeu----- 225
  |||
  |||
  |||
Db 824 TTTACCCATATCTTAGCTTTGAATTAAATATMAAGTAACTGAGTGGCACTGTGCT 883
QY 225 ----- 225
  |||
  |||
  |||
Db 884 CTTGTTCTGCGCTTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGGAT 943
QY 225 ----- 225
  |||
  |||
  |||
Db 944 AAGTCTCATAGTATATATGATTAATATACTGAGATAATACCTTCACACATTGACTCAGCAC 1003
QY 225 ----- 225
  |||
  |||
  |||
Db 1004 ACCAGGTATGTCAACAATTGTGCTTTTGACCTAATACCTTTTACTTGCTACTGCTTCA 1063
QY 226 ----- 226
  |||
  |||
  |||
Db 1064 ATGAGACAAAACAGTGAACATCTGGCAATTGGACCTGGAAACACTTGGCCAAAGCAGAGAGC 1123
QY 229 ThrGluHisGlnLeuValGlnPheThrGluAspTyrSerGluGluValIleSerThrTyr 248
  |||
  |||
  |||
Db 1124 ACAGAACATCAGCTGAAGCAATTTTACCGAAGATTTGGCAGAGGAGATGTCTCAACATCG 1183
QY 249 LeuCyAlaIleAspLeuValGlyIlePheIlePheMetAsnAsnIleAspGly 268
  |||
  |||
  |||
Db 1184 CTTTGTCACAAAGATTTTAAAGATCTTGTGATTTTCAAGATGAATTAACATTGATGGA 1243
QY 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
  |||
  |||
  |||
Db 1244 AAGAACTGTGAATCTTACAAAGAAAGTCTGGCTCATATTGAAATTTGAATCTCTA 1303
QY 289 GlyLeuArgSerLysValLeuValGlyIleGluGlnLeuArgThrLysValLysSerLeu 308
  |||
  |||
  |||
Db 1304 GGACTGCGTGTAAAGCTGAGGAAATTTGAAGAGCTCAGAGCAACAAAGTTAAATCCCTT 1363
QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
  |||
  |||
  |||
Db 1364 TCTTCAGAAATCTCTGATGAATTTATATGTCACATACTAGAGAACTTAAGAAAGATCCG 1423
QY 329 ValIleAlaSerAspGlyTyrSerTyrGluLysGluIleMetGluAsnTyrIleSerLys 348
  |||
  |||
  |||
Db 1424 GTCATCCCATCAGATGGCTATTCATATGAAAGAAAGCAATGAAATTTGATCAGCAAA 1483
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleThrProAsn 368
  |||
  |||
  |||
Db 1484 AAGAAACGTCAAGTCCCATGACAAATCTTGTCTTCCAGCGGTATTAACCAAT 1543
QY 369 ArgThrLeuLysMetAlaIleAsnArgTyrLeuGlnIleThrHisGlnLys 384
  |||
  |||
  |||
Db 1544 AGGACTGTGAATAATGGCCATCAATAGATGGCTGAGACACACAAAG 1591
RESULT 10
ADQ99098 ID ADQ99098 standard; cDNA; 1844 BP.
XX AC ADQ99098;
XX 23-SEP-2004 (first entry)
XX DNA encoding human GPCR-like protein seqid 768.
XX ophthalmological; immunomodulatory; cyrostatic; antiatherosclerotic;
XX anti diabetic; GPCR-like protein; ophthalmic disorder;
XX neurological disorder; immunological disorder; nephritic disorder;
XX hormonal dysfunction; cancer; atherosclerosis; diabetes;
XX molecular weight marker; food supplement; human; ss.
XX Homo sapiens.
XX
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XX XX
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XX US6569662-B1.
XX
XX
XX 27-MAY-2003.
XX
XX 19-JUL-2000; 2000US-00620312.
XX
XX 21-JAN-2000; 2000US-00489725.
XX
XX 25-APR-2000; 2000US-00552317.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Zhou P, Dymnac RT;
XX
XX WPI; 2001-442255/47.
XX
XX New G-protein-coupled receptor-like polypeptides and polynucleotides,
XX useful for treating diseases of ophthalmic, neurological, immunological
XX and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
XX and diabetes.
XX
XX Example 2; SEQ ID NO 768; 92pp; English.
XX
XX The invention describes an isolated polynucleotide (I) comprising a fully
XX defined (SI) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041,
XX 1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as
XX given in the specification, its translated or protein coding portion, its
XX extracellular portion or its active domain. The GPCR-like polypeptides
XX and polynucleotides are useful for the treatment of diseases of
XX ophthalmic, neurological, immunological and nephritic systems. They may
XX also be used to treat hormonal dysfunction, cancer, atherosclerosis and
XX diabetes. The antibodies are useful for detecting or quantitating the
XX polypeptide in tissue. The polypeptides can also be used as molecular
XX weight markers and as a food supplement. This sequence represents a human
XX polynucleotide of the invention.
XX
XX SQ Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other:
XX
XX Alignment Scores:
XX Pred. No.: 1,428-184 Length: 1844
XX Score: 1978.00 Matches: 382
XX Percent Similarity: 80.25% Conservative: 0
XX Best Local Similarity: 80.25% Mismatches: 2
XX Query Match: 96.63% Indels: 92
XX DB: 5 Gaps: 1
US-10-077-111-13 (1-384) x ADQ99098 (1-1844)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
  |||
  |||
  |||
Db 164 ATGATGAACCTGATTCACACATTAGCTGATGTCGAGATGTCANCTGCTGCTTTC 223
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgCysLysLeuArg 40
  |||
  |||
  |||
Db 224 TCTTTTCCCTCTTGCTACTGCTCTCTCTTGACAAACAATTCGCTGTACGTACGT 283
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
  |||
  |||
  |||
Db 284 GACTTACTGAAGTGCACATTTCTCATTTGAAGTTTCAATCCATCTCTCCATCTCTCG 343
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
  |||
  |||
  |||
Db 344 TGTTCCTCCCTTCAGAGACATATTTTGGCATGCTGTTCAAACAGATGTGTCACACTGTCTTA 403
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
  |||
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  |||
Db 404 TGGAAATCTGAATAATGACAGATGTCGACAGTGAAGAACAGCTAGTGGCAGCCCTGTG 463
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyValAlaAspGlyThr 120
  |||
  |||
  |||
Db 464 AGGGTTTGCAGATTTTCCCAAGCTCCACAGTGTGTTGGATCAGGGGCACTGATGGAAGT 523
QY 121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
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Db 524 GTGCTTTTGTCAGATGCACAGTCATACAAATTAATATGATGTGTAAGTAAAGATGC 583
Qy 141 SerLeuAlaAlaCysAlaPheSerProbsnGlySerPhePheValThrGlySerSerCys 160
Db 584 TCCCTTGGCGGCGATGTCATTTTCTCTAATGGAAGCTTCTTGTCCAGCTGCTCTCATGT 643
Qy 161 GlyAspLeuThrValTTPAspAspLysMetArgCysLeuHisSerGlyValAlaHisAsp 180
Db 644 GGTGATTTAAACAGTGTGGATGATPAAATGAGGTGTGCAATGATGTAAGCAACATGAT 703
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 704 CTTCGAATTACTCTGCTGCGATTTTCTTCCACAGCAGTTTCTGATGAGAAACAAGTCTT 763
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTyrIleValSer 220
Db 764 CAGTTTTTTCCAGTCGCGCATCATGTGTGTCAGGATTCGCAAAATTTGGATTGTTTCT 823
Qy 221 PheThrHisIleLeu----- 225
Db 824 TTACCCCATATCTTAGGTTTGAATPAAATATPAAAGTACACTGAGTGGCACTGTGCT 883
Qy 225 ----- 225
Db 884 CCTGTTCTGCGTGTGCTTTTCCCATGATGGGAGAGATGCTAGTCTCAGGCTCAGTGAT 943
Qy 225 ----- 225
Db 944 AAGTCTGTCATAGTATATGATATACTAATACTAGAGATAATACTTACACATGACTCAGCAC 1003
Qy 225 ----- 225
Db 1004 ACCAGGATATGCACAACATTGTCTTTGCACTTAATACCTTTACTTGTCTACTGTTC 1063
Qy 226 -----AlaArgArg 228
Db 1064 ATGCACAACACAGTCAACATCTGCGCAATTTCACCTCGAAACAATTGGCAACAGAGAGC 1123
Qy 229 ThrGlnHisGlnLeuLysGlnPheThrGlnAspTyrSerGlnGluValValSerThrTyr 248
Db 1124 ACAGAACTCAGCTGAGGCAATTTACCGAAGATTGTGTGAGAGAGAGATGTCTCAACATGG 1183
Qy 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db 1184 CTTGTGTCACAAGATTAAAGATCTGTGTGTAATTTTCAAGATGAATPACATTTGATGGA 1243
Qy 269 LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu 288
Db 1244 AAAAAGACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAAATTTGAATCTTA 1303
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
Db 1304 GGACTGCGTACTAAAGTGTGAGGAAAATGTAAAGAGCTCAGAGCAACAAAGTTAAATCCCTT 1363
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db 1364 TCTTCAGGAATTTCCGATGAAATTATATATGTCCAATPACTAAGAACTTATATAAAGATCG 1423
Qy 329 ValIleAlaSerAspGlyTyrSerTyrGlnLysGlnAlaMetGlnLysTyrIleSerLys 348
Db 1424 GTCATCCGATCAGATGGCTATTTCAATGAAAAGAAAGAAAGTGAATAATGATCAGCAA 1483
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1484 AAGAAACCTACAAAGTCCCATACAAATCTGTCTTCTTCCCTCAGCGGTACTTACACCAAT 1543
Qy 369 ArgThrLeuLysMetAlaIleAsnArgThrLeuGluThrHisGlnLys 384
Db 1544 AGGACTCTGAAAATGCGCATCATATGATGCTGAGACACACCAAAAG 1591

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ID ADB48858 standard; cDNA; 1844 BP.
XX
AC ADB48858.
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA seq ID NO 768.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PE 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
XX (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUND/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
XX
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX
DR WPI; 2003-678194/64.
XX
XX New polynucleotide, useful for treating diseases e.g., cancer or
PT neurodegenerative diseases.
XX
PS Claim 1; SEQ ID NO 768; 99pp; English.
XX
CC The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,
CC cancer or neurodegenerative diseases and many others listed in the
CC specification. The present sequence represents a novel human cDNA. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPRO
CC at seqdata.uspto.gov/sequence.html?docid=20030104529.
XX
SQ Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,42e-184 Length: 1844
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: Gaps: 1
US-10-077-111-13 (1-384) x ADB48858 (1-1844)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValaAsnCysCysAlaPhe 20
Db 164 ATGTGAAAGATGATTCACACATTTAGTATGATCATGTGACGATGCAACTGCTGCTTTC 223
Qy 21 SerPheSerLeuLeuAlaThrCysSerSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
Db 224 TCCCTTTCCCTCTGCTGCTACTGCTCTCTTGACAAAACAATTCGCTGTACTGTTACGT 283
Qy 41 AspPheThrGlnLeuPProHisSerProLeuLysPheHisThrTyrAlaValaHisCysCys 60
Db 284 GACTTTACTGACAGCCACATTTCTCCATTTGAAGTTTATATACATGCTGTCCATGCTGCG 343
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 344 TGTTCCTCCCTTCAGACATATATTTTGGCATCGTGTCAACACAGATGCTACCATGCTCTTA 403

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QY 81 TTPAsnThrcGluAengIyGImocUleuAlaValMeGluGInProserGIySerProval 100
| | | | |
Db 404 TGGAAATACtAAAAATGACAGATGCTGGCAGTATGAGAACACCTACTGGCAGCCCTGTG 463
QY 101 ArgValCysGInPheSerProaspSerThrcysleuAlaSerGIyAlaAaspGIyThr 120
| | | | |
Db 464 AGGGTTGGCCAGTTCCTCCAGACTCCAGCTGTTGGCATCAGGGGAGCTGATGAACT 523
QY 121 ValValleuThrcPheAnaGInserThrcysleuValThrcysGlySerValLyAspGly 140
| | | | |
Db 524 GTGGTTTGGGAGATGACAGTCAATACAAATATATGATGATGATGTTAAAGATGSC 583
QY 141 SerleuAlaAlaCysAlaPheSerProaspGIySerPhePheValThrcIySerSerCys 160
| | | | |
Db 584 TCCTGGCGGAGTGTGATTTCTCCAAATGGAAGCTTTCTTGTCATGGCTCCTCATGT 643
QY 161 GlyAspLeuThrcValTTPAspAspLyMetArgCysleuHisSerGIyLyAlaHisAsp 180
| | | | |
Db 644 GGTGATTTAAcAGTGTGGATGATMAAATGAGGTGTCTGATAGTGAATAAGCACATGAT 703
QY 181 leuGIyIleThrcCysAspPheSerSerGIyProvalSerAspGIyGluGInGlyLeu 200
| | | | |
Db 704 CTGGAAATACCTGGCTGGCAATTTCTTCCACAGCAATTTCTGATGGAGAACAGGCTCT 763
QY 201 GlnPhePheArgleuAlaSerCysGIyGlnAspCysGlnValLyIleTPIleValSer 220
| | | | |
Db 764 CAGTTTTTGCAGCTGGCATGTGTGTCAGATTGGCAAGCAAAATTGGATTGTTCT 823
QY 221 PheThrcHisIleleu----- 225
| | | | |
Db 824 TTTACCCATATCTTAGGTTTGAATTAAAAATATAAGTACACTAGTGGGCACTGTGCT 883
QY 225 ----- 225
| | | | |
Db 884 CCGTTCTGCTGTGCTTTTCCCATGATGAGGAGATGCTAGTCTCAGGAGTACGTGAT 943
QY 225 ----- 225
| | | | |
Db 944 AAGCTGTCAATGATATGATACTAATACAGAGAATATACTTCAcACATGACTCAGCAC 1003
QY 225 ----- 225
| | | | |
Db 1004 ACCAGTATGTCAcACACTGTGCTTTGGCACTTAATACCTTTTACTGCTACTGTTCA 1063
QY 225 ----- 225
| | | | |
Db 225 ----- 225
| | | | |
QY 226 ----- 228
| | | | |
Db 1064 ATGGACAAAACAGTGAACATCTGGCAATTGGACCTGGAAACACTTGGCCAAAGAGAGC 1123
QY 229 ThrcGluHisGlnleuLyGlnPheThrcGluAspTTPserGIyGluValValIserThrcTTP 248
| | | | |
Db 1124 ACAGAACATCAGCTGAAGCAATTTACCGAAGATTGGTCAGAGGAGATGTCCTCAACATGG 1183
QY 249 leuCyAlaGlnAspLeuLyAspLeuValGIyIlePheLySMeCAnaAnIleAspGly 268
| | | | |
Db 1184 CTTTGTGCACAAAGATTMAAAGACTTGTGTGATTTTCAAGATGAATAACATTGATGAGA 1243
QY 269 LyGluIleuLeuAnleuThrcLyGluSerleuAlaAspAspLeuLySIIeGluSerleu 288
| | | | |
Db 1244 AAGGAACCTGTTGAATCTTACAAAGAAAGTCTGGCTATGATTTGAAATTTGAATCTCTA 1303
QY 289 GlyleuArgSerLyValIleuArgLySIIeGluIleuArgThrcLyValLySIIeSerleu 308
| | | | |
Db 1304 GGAAGCTGTGTAAGAGCTGAGAGAAATTTGAAGAGCTCAGAGCAAGGTTAAATCCCTT 1363
QY 309 SerSerGIyIleProAspGluPheIleCysProIleThrcArgGluLeuMetLyAspPro 328
| | | | |
Db 1364 TCTTCAGGAATTCCTGATGAAATTAATATGTCATATACTGAGAAACTTATCAAAAGATCCG 1423
QY 329 ValIleleAspArgLyIleProAspGluPheIleCysProIleThrcArgGluLeuMetLyAspPro 348
| | | | |
Db 1424 GTCATCCATCAGATGAGCTATTCTATATGAAGAAGAAAGCAATGGAAATTTGATCAGCAA 1483

QY 349 LysLyArgThrcSerProMetThrcPheLeuValleuProSerAlaValleuThrcProAn 368
| | | | |
Db 1484 AAGAAACGTACAAAGTCCCATGACAAATCTGTTCTTCTTCCAGCGGTACTTACACCAAAAT 1543
QY 369 ArgThrcLeuLyMetAlaIleAnaArgTTPleuGluThrcHisGlnLyS 384
| | | | |
Db 1544 AGGACTCTGAAATGGCCATCATATAGATGCTCGAGACACACCAAAAG 1591
RESULT 12
AAd45076
ID AAd45076 standard; DNM; 1908 BP.
AC AAd45076;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human RET16.3 splice variant DNM.
XX
KW Human; RET16; intracellular signal; inflammation-related disease; asthma;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
KW transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KW inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
KW inactive respiratory distress syndrome; cardiac; ulcerative colitis;
KW autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
KW cellular migration disorder; cell proliferation disorder; calcification;
KW hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
KW cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KW thalassemia; vasotropic; gene; ds.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT 136..1644
FT CDS /tag= a
FT /product= "Human RET16.3 splice variant protein"
XX
XX MO200266494-A2.
XX
XX 29-AUG-2002.
XX
XX
XX 15-FEB-2002; 2002MO-US005162.
XX
XX 16-FEB-2001; 2001US-0269366P.
XX 29-MAY-2001; 2001US-0294181P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Todderud CG, Finger JN, Rillema J;
XX
XX WPI; 2002-682760/73.
XX P-PSDB; AAE28168.
XX
XX New human, mouse or rat RET16 gene and proteins, involved in
PT intracellular signaling cascade, useful for in gene therapy, particularly
PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancer,
PT tumors or neoplasms.
XX
XX
XX Claim 1; Page 168-169; 175pp; English.
XX
XX The invention relates to human, mouse or rat RET16 genes and proteins,
XX involved in intracellular signaling cascade. The RET16 protein or
XX polynucleotide is useful for treating an inflammation-related disease or
XX disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
XX asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
XX tissue transplants, chronic obstructive pulmonary disease, inflammatory
XX bowel disease, Crohn's disease, ulcerative colitis, inactive respiratory
XX distress syndrome, systemic lupus erythematosus, autoimmune disease,
XX cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
XX disease or disorder also includes disorders associated with aberrant
XX activation of the TNF-alpha pathway, disorders associated with aberrant
XX cellular migration, proliferation, metastasis, juvenile idiopathic
XX arthritis, haematogenous metastases of tumour cells, hyperinsulinaemia,
XX diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,

PI Mao Y, Xie Y;
 XX WPI: 2001-537038/60.
 DR P-PSDB; AAG78660.
 XX
 PT New polypeptide-beta-transducin 41 for treating e.g. cancer and HIV
 PT infection.
 XX
 PS Claim 6; Page 24-25 (Disclosure); 32pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of beta-
 CC transducin 41. The sequences can be used in the treatment of cancer and
 CC HIV infection. The present sequence is the coding sequence of the
 CC invention
 XX
 SQ Sequence 1623 BP; 485 A; 302 C; 335 G; 501 T; 0 U; 0 Other;

Alignment Scores:

Prod. No.: 1,96e-172 Length: 1623
 Score: 1854.00 Matches: 364
 Percent Similarity: 79.18% Conservative: 1
 Best Local Similarity: 78.96% Mismatches: 2
 Query Match: 90.57% Indels: 94
 DB: 4 Gaps: 1

US-10-077-111-13 (1-384) x AA164914 (1-1623)

QY 18 CysAlaPheSerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyr 37
 Db 3 TGGCCCTTCCTCCCTTCCCTTGGCTGCTGCTGCTGCAAAACAAATTCGCTGTAC 62
 QY 38 SerLeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaVal 57
 Db 63 TCGTTAGCTGACTTACTTGAATGCCAATTCCTCATTTGAAGTTCTACTATGCTGCTC 122
 QY 58 HisCysCysAspPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThr 77
 Db 123 CACGCGCTGCTTCTCCCTTCAGGACATATTTGGCATGCTGTTCAACAGATGTACC 182
 QY 78 ThrValLeuThrPheSerThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGly 97
 Db 183 ACTGCTCTTAAGAACTGAAATGAGACAGATGCTGCGAGATGAGAAACCTTAGTGGC 242
 QY 98 SerProValArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAla 117
 Db 243 AGCCCTGTGAGGGTTTCCCACTTTCCCAAGCTCCACGCTTTGGCATCAGGGCAGCT 302
 QY 118 AspGlyThrValValLeuThrPheAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerVal 137
 Db 303 GATGGAACGTGGCTTTGTGGAATGACACAGTCATACAAATTAATATGATGTGGTAGTGT 362
 QY 138 LysAspGlySerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGly 157
 Db 363 AAGATAGCTCTCTGGGGGCGATGTCATTTCTCTTAATGGAACCTTCTTTGCTACCTGGC 422
 QY 158 SerSerCysGlyAspLeuThrValTyrAspAspLysMetArgCysLeuHisSerGlyLys 177
 Db 423 TCCCATGTGGTGTATTAACAGTGTGGAGATGAATGAGGTCTCTGCATATGGAAAA 482
 QY 178 AlaHisAspLeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlu 197
 Db 483 GCACATATGCTTGAAATTAACCTGCTGCGATTTTCTTCACAGCCAGTTTCTGATGGAGAA 542
 QY 198 GlnGlyLeuGlnPhePheAspArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTyr 217
 Db 543 CAAGGCTTTCAGTTTTCGACGTGACATCATGTGTGTCAGGATTCGCAAGTCAAAAATTTGG 602
 QY 218 IleValSerPheThrHisIleLeu----- 225
 Db 603 ATTGTTCTTTTACCAATATCTTAGGTTTGAATTAATAATAAAGTACACTGAGTGG 662
 QY 225 ----- 225

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 QY 225 ----- 225
 Db 723 TCAGTGATTAAGTCTGTCTATAGTATATGATTAATTAATGAGAAATTACTTACACATTG 782
 QY 225 ----- 225
 Db 783 ACTCAGACACACAGATATGTACACAACTGTGCTTTTGCACTTAATACCTTTTACTTGCT 842
 QY 225 ----- 225
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 QY 226 AlaArgArgThrGlnHisGlnLeuLysGlnPheThrGlnAspThrProSerGlnGluVal 245
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 Db 1263 ATCAGCAAAAAGAAAGCGTACCAAGTCCCATGACCAATCTTGTCTTCCCTTCAAGCGGCT 1322
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 KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager syndrome; chemoactive;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukemia; ss.
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 XX
 PN W020015312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.

QY 384 s 384
Db 262 A 262

RESULT 15
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ID ADM19385 standard; cDNA; 1686 BP.
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AC ADM19385;
XX
DT 20-MAY-2004 (first entry)
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DE Novel human channel/transporter gene #182.
XX
KW da; gene; immunosuppressive; antiarthritic; antirheumatic;
KW antiapoptotic; cytosolic; cardiac; vasotropic; cerebroprotective;
KW neurotrophic; neuroprotective; antibacterial; vituicide; fungicide;
KW optalmological; gene therapy; channel/transporter protein;
KW rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder;
KW cerebral ischemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.
XX
OS Homo sapiens.
XX
PN WO200154472-A2.
XX
PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US001307.
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PR 04-FEB-2000; 2000US-0180628P.
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PR 02-MAR-2000; 2000US-0186350P.
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PR 17-NOV-2000; 2000US-0249216P.

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QY	329	ValIleAlaSerAspGlyTyrSerTyrGluLysGluAlaMetGluAsnTrpIleSerLys	348
Db	1281	-----GATGCTATTCTATGAAAAGGAAAGCAATGGAAATTGGATCAGCAAA	1328
QY	349	LysLysaArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn	368
Db	1329	AAGAAAGTACAGTCCCATGACAAATCTGTCTTCCTTCAGCGGTACTTACACCAAT	1388
QY	369	ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys	384
Db	1389	AGGACTCTGAAAATGGCCATCAATAGATGGCTGGAGACACACCAAAAG	1436

Search completed: October 25, 2005, 02:15:57
Job time : 512 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 04:11:04 ; Search time 3795 Seconds
(without alignments)
16241.116 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: gb_om: *
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13: gb_un: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	964.2	75.8	1844	9	AR339277 Sequence
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4	893.4	70.2	1919	6	AK123983 Homo sapi
5	890.2	70.0	1811	6	AK1748164 Sequence
6	890.2	70.0	1811	9	AK093494 Homo sapi
7	878.8	69.1	1996	6	CO491312 Sequence
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9	478.6	37.6	1291	6	AX077675 Sequence
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11	436	34.3	1547	10	BC050792 Mus muscu
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15	335	26.1	366	6	CO096643 Sequence
16	331.6	26.1	366	6	CO135438 Sequence
17	331.6	26.1	366	6	CO218732 Sequence
18	331.6	26.1	366	6	CO294537 Sequence
19	331.6	26.1	366	6	CO294537 Sequence

C 20	331.6	26.1	366	6	CO331208	CO331208 Sequence
C 21	329.8	25.9	409	6	CO482331	CO482331 Sequence
C 22	328.8	25.8	441	6	CO503452	CO503452 Sequence
C 23	328.8	25.8	441	6	CO512287	CO512287 Sequence
C 24	297	23.3	297	6	CO109842	CO109842 Sequence
C 25	297	23.3	297	6	CO148540	CO148540 Sequence
C 26	297	23.3	297	6	CO231810	CO231810 Sequence
C 27	297	23.3	297	6	CO307124	CO307124 Sequence
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C 30	276.8	21.8	315453	2	AC122070	AC122070 Rattus no
C 31	275.4	21.7	196403	2	AC102767	AC102767 Mus muscu
C 32	275.4	21.7	209437	2	AC111119	AC111119 Mus muscu
C 33	275.4	21.7	217352	10	AL929242	AL929242 Mouse DNA
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C 39	179.6	14.1	466	6	CO332079	CO332079 Sequence
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C 41	176.8	13.9	180	6	CO110706	CO110706 Sequence
C 42	176.8	13.9	180	6	CO149443	CO149443 Sequence
C 43	176.8	13.9	180	6	CO232723	CO232723 Sequence
C 44	176.8	13.9	180	6	CO270754	CO270754 Sequence
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ALIGNMENTS

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AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
USA

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BC029520
BC029520.1 GI:20810486
MGC.
Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Srausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Adams, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, X., Gibbs, R.A.,
Vallion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Raney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzyzinski, M.I., Skalski, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1564)
Srausberg, R.
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshiyuki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 48 Row: 0 Column: 11
This clone was selected for full length sequencing because it
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ORIGIN

Query Match. 98.3%; Score 1250.2; DB 9; Length 1564;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1212 AATAGACTCTGAAATGGCCATCAATAGATGCTGGAGACACACCAAAAGTAA 1266
1247 AATAGACTCTGAAATGGCCATCAATAGATGCTGGAGACACACCAAAAGTAA 1301

RESULT 2
AR339277 1844 bp DNA linear PAT 17-AUG-2003
LOCUS AR339277
DEFINITION Sequence 768 from patent US 6569662.
ACCESSION AR339277
VERSION AR339277.1 GI:33726134
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown:
Unclassified.
REFERENCE 1 (bases 1 to 1844)
AUTHORS Tang, Y.T., Zhou, P. and Dermanac, R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 659662-A 768 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..1844
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/mol_type="genomic DNA"

ORIGIN

Query Match 75.8%; Score 964.2; DB 6; Length 1844;
Best Local Similarity 81.8%; Pred. No. 2,6e-250;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

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DB 125 CCCCCGCTCCGCGCGCTTTTCTTCAATAAAGAAACATGGTGAACGATCAGACA 184
QY 132 TTACCTGATCATGCTGACGATGTCACGCTGCTCTTCTTCCCTTGGCTACT 191
DB 185 TTACCTGATCATGCTGACGATGTCACGCTGCTCTTCTTCCCTTGGCTACT 244
QY 192 TGCTCTTGACAAACAAATTCGCTGCTGTTACGTCGATCTTGAACCTGCCA 251
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QY 432 GACTCCACGTTTGGGATCAGGGGCGACGCTGATGGAACGTTGGTGGTGG 491
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QY 672 TTTTCTTCAAGCAGTTTCTGATGAGAACAGGCTTCTAGTTTTCGACTGGCA 731
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QY 785 ----- 784

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DB 1025 GCTTTGACCTAATACCTTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
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DB 1565 AATGATGCTGAGAGACACCAAAAGTAAA 1595

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RESULT 3
CQ729621 1254 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15555 from Patent WO02068579.
ACCESSION CQ729621
VERSION CQ729621.1 GI:42301208
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
theretof
JOURNAL Patent: WO 02068579-A 15555 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
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ORIGIN

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Db	345	TTGGACAAAACAAATTGGCTGTACTGTTTACGTGACTTTACTGAACTGCCAATTCTTCCA	404
OY	258	TTTGAAGTTTCACTACTATGCTGTGCACCTGCTGCTTTTCTCCCTTCAGAACATATTYTG	317
Db	405	TTTGAAGTTTCACTACTATGCTGTGCACCTGCTGCTTTTCTCCCTTCAGAACATATTYTG	464
OY	318	GCATCGTGTTCAACAGATGTGTACCACTGCTCCATATGGAAATPACGAAAAATGACAGATGCTG	377
Db	465	GCATCGTGTTCAACAGATGTGTACCACTGCTCCATATGGAAATPACGAAAAATGACAGATGCTG	524
OY	378	GCAGTGTATGGAACAGCCCTAGTGGGACGCCCTGTGAGGGTTTGGCAGTTTCCCGACACTCC	437
Db	525	GCAGTGTATGGAACAGCCCTAGTGGGACGCCCTGTGAGGGTTTGGCAGTTTCCCGACACTCC	584
OY	438	ACGCTGTTGGCATCAGGGGGCAGCTGTATGGAACCTGTGTTTGTGTGAATGCAACGTCATAC	497
Db	585	ACGCTGTTGGCATCAGGGGGCAGCTGTATGGAACCTGTGTTTGTGTGAATGCAACGTCATAC	644
OY	498	AAATTATATTAATGTGGTATGTAAATAATGGCTCCTTGGGGGACATGCAATTTTCTCCT	557
Db	645	AAATTATATTAATGTGGTATGTAAATAATGGCTCCTTGGGGGACATGCAATTTTCTCCT	704
OY	558	AATGGAAGCTCTTGTGCTACTGGCTCCTCATGTGGTATTTTAAACAGTGTGGAAATGATAAA	617
Db	705	AATGGAAGCTCTTGTGCTACTGGCTCCTCATGTGGTATTTTAAACAGTGTGGAAATGATAAA	764
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Db	765	ATGAGTGCTGTGCATAGTGAATAAGCAATGATCTTGGAAATTAACCTGCTGCAGATTTTCT	824
OY	678	TCACAGCCAGTTTCTGATGAGGAACAAAGTCTTCAAGTTTTCATCTGGCATCATGTGCTG	737
Db	825	TCACAGCCAGTTTCTGATGAGGAACAAAGTCTTCAAGTTTTCATCTGGCATCATGTGCTG	884
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Db	885	CAGAGTTGCCAAGTCAAAATTTGGATTGTTCTTTTACCCTATCTTAGGTTTGAATTA	944
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Db	945	AAATATATAAAGTACACTGATGGGCACTGTGCTCCTGTTCTGGCTGTGCTTTTCCCAT	1004
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Db	1005	GATGGCAGATGCTAGTCTCAGGGTCAGTGGATATAGTCTGTCAATATATGATATCTAAT	1064
OY	785	-----	784
Db	1065	ACTGAGAAATATACCTTACACAACTTGACTAGCAACACAGGTATGTCAACAATTTGCTTTT	1124
OY	785	-----	784
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Db	1185	TTTGCACCTGAAAAACATTTTGCCAAAGCAAGGAGCACAGAAACATCTGACAAATTTTACC	1244
OY	822	GAAATTTGGTTCAGAGGAGGTGGTGTCAACATGGGCTTTTGTGACAAAGATTTTAAAGATCTT	881
Db	1245	GAAATTTGGTTCAGAGGAGGTGGTGTCAACATGGGCTTTTGTGACAAAGATTTTAAAGATCTT	1304
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Db	1305	GTTGGTATTTTCAAGATGAATTAACATTTGATGGAAAAAGAACTGTGAATCTTTTACAAAGAA	1366
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Db	1365	AGTGTGGCTGATGATTGGAAATTGAATCTCTAGAGACTGGGTAGTAAAGTGTGAGAAA	1424
Qy	1002	ATTGAAAGAGCTCAGACCAAGTTAAATCCCTTTCTTCAGAAATTCCTGATGAATTTATA	1061
Db	1425	ATTGAAGAGCTCAGAGCAAGGTTAAATCCCTTTCTTCAGGAATTCCTGATGAATTTATA	1484
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Qy	1122	GAAGAAGAGCAATGAGAAAATTGGATCAGCAAAAAGAAAGCTACAGATCCCATGACAAAT	1181
Db	1545	GAAGAAGAGCAATGAGAAAATTGGATCAGCAAAAAGAAAGCTACAGATCCCATGACAAAT	1604
Qy	1182	CTTGTTCTTCCTTCAGCGGTACTTACACCAAAATGAGACTGTGAAATGGCCATCAATAGA	1241
Db	1605	CTTGTTCTTCCTTCAGCGGTACTTACACCAAAATGAGACTGTGAAATGGCCATCAATAGA	1664
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Db	1665	TGCGTGGAGACACACCAAAAGTAAA	1689
RESULT 5			
LOCUS	AX748164	1811 bp	mRNA
DEFINITION	Sequence 1689 from Patent EPI308459.	linear	PAT 20-JUN-2003
ACCESSION	AX748164		
VERSION	AX748164.1	GI:32132552	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuko,Y.		
TITLE	Full-length cDNA sequences		
JOURNAL	Patent: EP 1308459-A 1689 07-MAY-2003;		
	Helix Research Institute (JP) ; Research Association for Biotechnology (JP)		
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Best Local Similarity	80.9% ; Pred. No. 3,2e-230 ;		
Matches 1178 ; Conservative	0 ; Mismatches 3 ; Indels 276 ; Gaps 1.		
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Db	125	GGCTGTTTTCTTCAATAAAGAAACATGGTGAACCTGATTCACACATTAGCTGATCATGG	184
Qy	146	TGAGGATGTCACATGCTGTGCTTCTCTCTTTCCCTCTTGCTACTTGCTCTTGGACAA	205
Db	185	TGAGGATGTCACACGCTGTGCTCTCTCTTTCCCTCTTGCTACTTGCTCTTGGACAA	244
Qy	206	AACAAATTCGCTGACTCGTTACGTGACTTATGAACTGGCACATTCCTCATTTGAAGTT	265
Db	245	AACAAATTCGCTGACTCGTTACGTGACTTATGAACTGGCACATTCCTCATTTGAAGTT	304
Qy	266	TCATACCTATGCTGTCCACTGCTGCTGTCTTCCCTTCAGACATATTTTGGCATCGTG	325
Db	305	TCATACCTATGCTGTCCACTGCTGCTGTCTTCCCTTCAGACATATTTTGGCATCGTG	364
Qy	326	TTCAACAGATGATCCACTGTGCTTATGGAATATCGAATAAGACAGATGCTGCGACATGAT	385

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 Db 425 GGAACGCCCTAGTGGACGCCCTGTGAGGGTTTCCGATTTTCCCGACATCCACGCTTT 484
 QY 446 GGCATGAGGGGACGCTGATGGAACCTGTGTTTGTGGAAATGACAGTCATACAAATTA 505
 Db 485 GGCATGAGGGGACGCTGATGGAACCTGTGTTTGTGGAAATGACAGTCATACAAATTA 544
 QY 506 TAGATGTGTAGTGTAAAGATGCTCTTGGCGGCATGTGCATTTCTCTTAATGGAAG 565
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 QY 566 CTTCCTTTGACAGGCTCTCATGTGGTAAATTAACGTGTGGAGATTAATGAGCTG 625
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 QY 785 ----- 1024
 Db 785 ----- 1084
 QY 1025 TACCCCTTTACTGCTACTGTTCAATGACAAAGAGTGAACATCTGGCAATTTGACCT 1084
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 AK093494
 VERSION
 AK093494.1 GI:21752384
 o1igo capping; file (full insert sequence).
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Futu, Y., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, T., Iihashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimura, M., Watanabe, M., Hirooka, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hoota, T., Kusano, J., Kanehori, K., Takahashi, Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuma, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohara, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Coto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumeagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeata, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Saeki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
 Complete sequencing and characterization of 21,243 full-length human cDNAs
 Nat. Genet. 36 (1), 40-45 (2004)
 JOURNAL
 PUBMED
 14702039
 REFERENCE
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 Ishibashi, T., Kanehori, K., Yoshida, M., Watanabe, S., Ishida, S., Ono, Y., Hoota, T., Hirooka, S., Murakami, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Oshima, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 1811)
 JOURNAL
 REFERENCE
 3
 Isogai, T. and Yamamoto, J.
 TITLE
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (FRI Team); 2-6-7 kazusa-kametari, Kisarazu, Chiba 292-0812, Japan

COMMENT

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

Source

Location/Qualifiers

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CDS

Query Match 70.0%; Score 890.2; DB 9; Length 1811;
 Best Local Similarity 80.9%; Pred. No. 3.2e-230;
 Matches 1178; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

ORIGIN

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 206 AACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265
 245 AACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
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 1250 GACACACCAAAAGTAA 1266
 1565 GACACACCAAAAGTAA 1581

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 LOCUS CQ491312
 DEFINITION Sequence 23179 from Patent WO0160860.
 ACCESSION CQ491312
 VERSION CQ491312.1 GI:41456931
 KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE AUTHORS TITLE	Schlegel, R., Endele, W.O. and Monahan, J.E. Genes differentially expressed in human prostate cancer and their use
JOURNAL	Patent: WO 0160860-A 23179 23-AUG-2001; Millennium Predictive Medicine, Inc. (US)
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source	1..1996 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Best Local Similarity	80.7%; Pred. No. 4e-227;
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QY	279 GTCCACTGCTGCTGTTTCTCCCTTCAGACATATTTGGCATGCTGTTCACACAGATGCT 338
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QY	339 ACCATGTCCTATGGAATATGAAATGACAGATGCTGGCAGTATGGAACAGCTTACT 398
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QY	579 GGCTCTCATGTGATGATTTAAACAGTGTGGATGATAAATGAGGTGTCTGCATATGTA 638
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QY	639 AAAGCACATGATCTTGGAAATACCTGTCTGCGATTTTCTTCCACAGCCAGTTTCTGATGA 698
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QY	699 GAACAAGGCTTCAGTTTTTTTGGATGTCATGATGATGATGATGATGATGATGATGATGAT 758
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QY	759 TGGATTTGTTCTTTTACCATACTT----- 784
DB	664 TGGATTTGTTCTTTTACCATACTTCTTAGGTTTGAATTTAAATATATAAAGTACCTGAGT 723
QY	785 ----- 784
DB	724 GGGACGTGTCTCTGCTTCTGGCTTGTGCTTTTCCATGATGGCAGATGCTACTTCA 783

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OY	785	-----	784
Db	904	GCTACTGTTCATGTGACAAACACGTGACATCTGGCAATTTTGACCTGAAACACTTTTGC	963
OY	785	--ACCAAGGGCGACAGAAACATTCAGCTCTGACCAATTTTCCCAAGATTTGTCAGAGAGATC	842
Db	964	CACACAAAGGGCGACAGAAACATTCAGCTCTGACCAATTTTCCCAAGATTTGTCAGAGAGAT	1023
OY	843	GTCTCAACATGGCTTTTGTGCACAAGATTTTAAAGATCTTGTGGATTTTTCAGATGAAT	902
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Db	1144	ATTGAATCTCTAGAGCTGCGCTAGTAAGTCTGAGGAAATTGAAAGCTTCAGACCAAG	1203
OY	1023	GTTTAAATCCCTTTCTTCAGGAATTCCTGATGAATTTTATGTCCCAATTAACCTAGAACTT	1082
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Db	1264	ATGAAGATCCGCTCATTCGCATCAGATGGCTATTCAATGAAAAAGAACATGGAAAT	1323
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Db	1444	TAAA 1447	
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DEFINITION	Sequence 29046 from Patent WO0160860.		
VERSION	CQ497179		
KEYWORDS	CQ497179.1 GI:4162815		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Schlegel R., Endege, W.O. and Monahan, J.E.		
AUTHORS	1		
TITLE	Genes differentially expressed in human prostate cancer and their		
JOURNAL	use		
FEATURES	Patent: WO 0160860-A 29046 23-AUG-2001;		
source	Millennium Predictive Medicine, Inc. (US)		
	Location/Qualifiers		
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	Query Match	69.1%;	Score 878.8;	DB 6;	Length 1996;	
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	Matches 1166;	Conservative	0;	Mismatches	2;	Indels 276; Gaps 1.
QY	99	CAAAATAAAGAACATGAGTGAAAACCTGATTACACACATTAGCTGCATCATGTCAGTGCATGTCCAAC	158			
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QY	219	TACTCGTAGTGAACCTTACTGAACTGCGACATTCCTGCATTGGAAGTTTCATACCAATGCT	278			
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QY	399	GGCAGCCCTGAGAGGGTTTTGCCAGTTTTCCCACAGTCCACAGTGTGTTGGCATCAGGGGCA	458			
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QY	459	GCTATGGAATCTGTGTTTTGTGGAAATGACAGTGCATPACAAATPATATAGATGTGTAGT	518			
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QY	579	GGCTCTTCATGTGTGATTAAACAGTGGGATGATTAATAAGAGTGTCTGCATGTGAA	638			
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QY	639	AAGCACATGATCTTGGAAATTAACGTCGCGCATTTTTTCTTACACAGCAGTTTCTGATGGA	698			
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QY	699	GAAACAAGTCTTCAGTTTTTTTTCGACTGCGCATCATGTGCTCAGAGTTGGCAAATCAAAAT	758			
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QY	759	TGATTTGTTTTTTTATCCCATATCTT-----	784			
Db	664	TGATTTGTTTTTTTATCCCATATCTTATGTTTTGAAATTAATAATAAAGTACACTGAGT	723			
QY	785	-----	784			
Db	724	GGGCACTGTGCTCCTGTTCTTGCGTTTGCTTTTCCATGATGGCAGATGCTAGTCTCA	783			
QY	785	-----	784			
Db	784	GGGTCAAGTGAATTAAGTCTGTCAATAGTATATGATATCTAATACTGAAATATATCTTACACA	843			
QY	785	-----	784			
Db	844	TTGACTCAGCACACGAGTATGTACAACTTGTGCTTTTGACACTAATACCTTTTACTT	903			
QY	785	-----	784			
Db	904	GCTACTGTTCAATGACAAAACAAGTGAACATCTGGCAATTTGACCTGGAAAACCTTGTGC	963			
QY	785	--AGCAAGGCCACAGAAATCATGCTGGAAGCAATTTACGSAAGATTGTCACAGAGAGTCC	842			
Db	964	CACGCAAGGCCACAGAAATCATGCTGGAAGCAATTTACGSAAGATTGTCACAGAGAGAT	1022			
QY	843	GTTCTCAACATGAGCTTTGTGCACACAGAATTTAAAGATCTTGTGTGATTTTCAAGATGAAT	902			

Db	1024	GTCCTCAACATGGCCTTTGTGCAAGATTAAAGATCTTGTGTATTTTCAMGATGAAT	1083
Oy	903	AACATGATGAAAAAAGAAGCTGTTGAACTCTTAACAAGAAAGCTCGCTGATGATTTGAAA	962
Db	1084	AACATGATGAAAAAAGAAGCTGTTGAACTCTTAACAAGAAAGCTCGCTGATGATTTGAAA	1143
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Db	1444	TAAA 1447	
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DEFINITION	Sequence 130 from Patent WO0105970.		
ACCESSION	AX077675		
VERSION	AX077675.1	GI:13122057	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	Xue,H., Tang,Y.T., Bandman,O., Hillman,J.D., Lai,P., Huo-Young,J.,		
	Reddy,R., Yang,J., Baughn,M.R., Lu,D.A., Azimzai,Y. and		
	Patterson,C.		
TITLE	Gep-binding protein associated factors		
JOURNAL	Patent: WO 0105970-A 130 25-JAN-2001;		
	Incyte Genomics, Inc. (US)		
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Beech Local Similarity	96.2%; Pred.No.1.ee-118;		
Matches 484; Conservative	0; Mismatches 9; Indels 0; Gaps 0;		
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Db	607	GAGAGAGATGCTCAACATGGCTTTGTGCACACAGATTTAAAGATCTTGTGGTATTTTC	666
Oy	894	AAGATGAATACATGATGAGAAAGAACTGTGTAATCTTCAAAAGAAAGCTGGCGAT	953
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ACCESSION BC061948
VERSION   BC061948
KEYWORDS  MGC:65547 GI:38303926
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2130)
AUTHORS  Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, J., Wang, J., Hsieh, F.,
Diatchenko, L., Marcina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheltz, T.E., Brownstein, M.J., Usdin, T.B., Tashyuk, S.,
Carninci, P., Prange, C., Raha, S.S., Loggiano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richardson, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Boutard, G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalski, U., Smalusz, D.E.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE 12477932
PUBMED 2 (bases 1 to 2130)
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE Submitted (10-NOV-2003) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs@email.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.

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FEATURES
source
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gatherersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hghl.nih.gov
Akher, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legabji, R.,
Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stancirp, S., Thomas, P.J., Touchman, J.W.,
Tsurgoun, C., Vogt, J.H., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 127 Row: 1 Column: 1
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analysis.

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JOURNAL

Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum,
Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
1, D-85764 Neuberg, GERMANY

FEATURES

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Location/Qualifiers

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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AUTHORS

TITLE

Submitted (26-FEB-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147021)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckert, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeBartellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G.,
Hagos, B., Heath, A., Horton, L., Howland, J. C., Jones, C., Kann, L.,
Karatas, A., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P.,
Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
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Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tessier, S., Tortorella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
Direct Submission
Submitted (03-FEB-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147021)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckert, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeBartellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G.,
Hagos, B., Heath, A., Horton, L., Howland, J. C., Jones, C., Kann, L.,
Karatas, A., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P.,
Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Naylor, J., Nijhoff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tessier, S., Tortorella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
Direct Submission
Submitted (26-FEB-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 1, 1999 this sequence version replaced gi:4309777.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
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JOURNAL

Patent: WO 0160860-A 5029 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES

source

Location/Qualifiers
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE	Schlegel, R., Endege, W.O. and Monahan, J.E.
JOURNAL	Genes differentially expressed in human prostate cancer and their use
FEATURES	Patent: WO 0160860-A 29046 23-AUG-2001; Millennium Predictive Medicine, Inc. (US)
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ACCESSION	AX748164		
VERSION	AX748164.1	GI:32132552	
KEYWORDS			
SOURCE			
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REFERENCE	Homo sapiens		
AUTHORS	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Euteleia; Primates; Catarrhini; Homnidae; Homo. 1		
	Isegorai,T., Sugiyama,T., Otsuki,T., Wakematsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Taneichi,K.I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahara,K. and Maehno,Y.		
TITLE	Full-length cDNA sequences		
JOURNAL	Patent: EP 1308459-A 1689 07-MAY-2003;		
	Helix Research Institute (JP) ; Research Association for Biotechnology (JP)		
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ORIGIN

Alignment Scores:

Pred. No.: 6,13e-172 Length: 1811
 Score: 1978.00 Matches: 382
 Percent Similarity: 80.25% Conservative: 0
 Best Local Similarity: 80.25% Mismatches: 2
 Query Match: 96.63% Indels: 92
 DB: 6 Gaps: 1

US-10-077-111-13 (1-384) x AX748164 (1-1811)

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ACCESSION AK093494
VERSION AK093494.1 GI:21752384
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Oca.T., Suzuki.Y., Nishikawa.T., Otsuki.T., Sugiyama.T., Irie.R.,
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TITLE	Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuno, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs		
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)		
PUBMED	14702039		
REFERENCE	2		
AUTHORS	Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Horiuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kuwano, Y., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuno, K., Nakamura, Y., Sekino, M., Kikuchi, H., Kanda, K., Magaruma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.		
TITLE	Unpublished		
JOURNAL	3 (bases 1 to 1811)		
REFERENCE	Isogai, T. and Yamamoto, J.		
AUTHORS	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7		
JOURNAL	Submitted Submission		
TITLE	Kazuo-Kamata, K., Katsura, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology (RAB) : cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation: clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.		
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DEFINITION Homo sapiens cDNA FLJ26473 fis, clone KDN04521.
ACCESSION AK129983
VERSION AK129983.1 GI:34526702
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
Fukushima, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H.,
Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,
Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,
Kawakami, B., Nagai, K., Isegai, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1919)
AUTHORS Sugano, S. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: fshcna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing; Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing; RAB; clone selection for
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Best Local Similarity: 80.25% Mismatches: 2
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DEFINITION      AJ719461      GI:53127473
ACCESSION      AJ719461.1      GI:53127473
VERSION      AJ719461.1
KEYWORDS      ORF1.
SOURCE      Gallus gallus (chicken)
ORGANISM      Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE      1      Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezubov, Y., Zaim, J.,
AUTHORS

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TITLE      Fiedler, P., Kuter, S., Biagodatetski, A., Kostovska, D., Koter, M.,
           Plachy, J., Carnici, P., Hayashizaki, Y., and Buerstedde, J.M.
           Full-length cDNAs from bursal lymphocytes to facilitate gene
           function analysis
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 3818)
AUTHORS      Caldwell, R.B.
TITLE        Direct Submission
JOURNAL      Submitted (20-MAY-2004) Caldwell, R.B., GSF - Forschungszentrum,
           Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
           1, D-85764 Neuberg, GERMANY
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Best Local Similarity: 58.91%      Mismatches: 62
Query Match:    71.52%      Indels:      94
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Qy      21      SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
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Qy      41      AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
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LOCUS         BC050792      2610014F08 gene, mRNA (cDNA clone
DEFINITION    IMAGE:6742025), partial cds.

ACCESSION    BC050792.1  GI:30048136
VERSION      BC050792.1
KEYWORDS     Mus musculus (house mouse)
SOURCE       Mus musculus
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 1547)
AUTHORS      Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
              Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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              Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smallov, D.E.,
              Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
              Generation and initial analysis of more than 15,000 full-length
              human and mouse cDNA sequences
              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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              TITLE
              JOURNAL
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              COMMENT
              REMARK
              CONTACT: MGC help desk
              Email: cgabs-remail.nih.gov
              Tissue Procurement: Dr. Jonathan Kuo, NIMH
              cDNA Library Preparation: Michael Brownstein / Ted Usdin
              USA-MGC Project URL: http://mgc.nci.nih.gov
              NIH-MGC Project URL: http://mgc.nci.nih.gov
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              Email: cgabs-remail.nih.gov
              Tissue Procurement: Dr. Jonathan Kuo, NIMH
              cDNA Library Preparation: Michael Brownstein / Ted Usdin
              laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA sequencing by: Genome Sequence Centre,
              BC Cancer Agency, Vancouver, BC, Canada
              info@cgsc.bc.ca
              Steven Jones, Jennifer Asano, Ian Boedec, Yaron Butterfield,
              Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
              Leticia Hehao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
              Sen Lee, Victor Ling, Carrie Mathewson, Kande McClavey, Steven
              Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saecodi, Jacquoline
              Schein, Duane Smallov, Michael Smith, Lorraine Spence, Jeff Sport,
              Michael Thorne, Miranda Tasi, Narasja van den Bosch, Jill Vardy,
              George Yang, Scott Zuyderduyn, Marco Marra.

clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 46 Row: a Column: 6
This clone was selected for full length sequencing because it
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Location/Qualifiers

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ORIGIN

Alignment Scores:

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US-10-077-111-13 (1-384) x BC050792 (1-1547)

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RESULT 12

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LOCUS AX077675
DEFINITION Sequence 130 from Patent WO0105970.
ACCESSION AX077675
VERSION AX077675.1 GI:13122057
KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE
AUTHORS
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Yue, H., Tang, Y. T., Bandman, O., Hillman, J. L., Lai, P., Au-Young, J.,
Reddy, R., Yang, J., Baughn, M. R., Lu, D. A., Azimzai, Y. and
Petersen, C.
TITLE
GTP-binding protein associated factors
JOURNAL
Patent: WO 0105970-A 130 25-JAN-2001;
Incyte Genomics, Inc. (US)
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Best Local Similarity: 71.10% Mismatches: 4
Query Match: 59.92% Indels: 93
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US-10-077-111-13 (1-384) x AX077675 (1-1291)

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QY 299 GlnGluLeuArgThrLysValLysSerLeuSerSerGlyIleProAspGluPheIleCys 318
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VERSION
KEYWORDS
HTG.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckely, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Deyayre, E., Devon, K., Dewar, K.,
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Funke, R., Gage, D., Galagan, J., Gardy, S., Gilbert, D., Grant, G.,
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Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
TITLE
JOURNAL
REFERENCE
AUTHORS
Submitted (03-FEB-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147021)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
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TITLE Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.
JOURNAL Direct Submission
COMMENT Submitted (26-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 1, 1999 this sequence version replaced gi:4309777.
All repeats were identified using RepeatMasker: Smt, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

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US-10-077-111-13 (1-384) x AC006501 (1-147021)

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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

Relly, B., Relly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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 Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von
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 Weissbrock, G. and Gibbs, R.A.

COMMENT

Submitted (17-SEP-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 245795)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 10, 2003 this sequence version replaced gi:24819739.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GFNB
 Center clone name: CH230-24D13
 ----- Summary Statistics
 Assembly program: Atlas 3.0,
 Consensus quality: 232948 bases at least Q40
 Consensus quality: 234943 bases at least Q30
 Consensus quality: 236332 bases at least Q20
 Estimated insert size: 240759; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_difft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

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US-10-077-111-13 (1-384) x AC096419 (1-245795)

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Qy	132	-----							
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Db	136242	TACTCTAAAGGATGTGTGTCAGCGTATAGCATCTGATCTTATTTGTAGGACCGGTCACT	136183						
Qy	132	-----							
Db	136182	CCTGGTCTGTACACGCCCGGTGTCTATTTCTAAAGGACGTATATAGAGTCCAAAGCTT	136123						
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DEFINITION	Rattus norvegicus clone CH230-18218, *** SEQUENCING IN PROGRESS								
ACCESSION	AC122070								
VERSION	AC122070.4	GI:25092709							
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 Weinstock, G., and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 315463)
 Direct Submission
 Worley, K.C.
 Direct Submission
 Submitted (22-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 315463)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 19, 2002 this sequence version replaced gi:23322130.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
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 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

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----- Project Information
Center project name: GMBU
Center clone name: CH230-18218
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 246672 bases at least Q40
Consensus quality: 252029 bases at least Q30
Consensus quality: 255877 bases at least Q20
Estimated insert size: 247533; sum-of-contigs estimation
Quality coverage: 5x in Q40 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html)
* NOTE: This is a "working draft" sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Percent Similarity:	731.00	Matches:	164
Best Local Similarity:	33.98%	Conservative:	10
Query Match:	32.03%	Mismatches:	20
	35.71%	Indels:	318
DB:	2	Gaps:	1
US-10-077-111-13 (1-384) x AC122070 (1-315463)			
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Job time : 4011 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 04:07:29 ; Search time 519 Seconds
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Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AC	AAD45075;
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DT	27-DEC-2002 (first entry)
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DE	Human RET16.2 splice variant DNA.
XX	
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KW	rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
KW	transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KW	inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
KW	infectious respiratory distress syndrome; cardiac; ulcerative colitis;
KW	autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
KW	cellular migration disorder; cell proliferation disorder; calcification;
KW	hyperinsulinemia; diabetes type 2; systemic lupus erythematosus; tumour;
KW	cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KW	thalassemia; vasotropic; gene; ds.
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FH	Key
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XX	WO200266494-A2.
XX	29-AUG-2002.
XX	15-FEB-2002; 2002WO-US005162.
XX	16-FEB-2001; 2001US-0269366P.
XX	29-MAY-2001; 2001US-0294181P.
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	Toddard CG, Finger UN, Rillema J;
XX	WPI; 2002-682760/73.
XX	P-PSDB; AAE28167.

XX New human, mouse or rat RET16 genes and proteins, involved in
PT intracellular signaling cascade, useful for in gene therapy, particularly
PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
PT tumors or neoplasms.
XX
PS Claim 1, Page 166; 175bp; English.
XX
CC The invention relates to human, mouse or rat RET16 genes and proteins,
CC involved in intracellular signaling cascade. The RET16 protein or
CC polynucleotide is useful for treating an inflammation-related disease or
CC disorder, e.g. Rheumatoid arthritis, juvenile arthritis, psoriasis,
CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
CC disease or disorder also includes disorders associated with aberrant
CC activation of the TNF-alpha pathway, disorders associated with aberrant
CC cellular migration, proliferation, metastasis, juvenile idiopathic
CC arthritis, haemogenous metastases of tumour cells, hyperinsulinaemia,
CC diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
CC tumour progression, Wegener's granulomatosis, stem cell transplantation
CC complications, ischaemia-reperfusion injury, thalassaemia, acute lung
CC injury, graft rejection, ischaemic heart, coronary artery calcification
CC or allergic inflammation. RET16 DNA is used in gene therapy. The present
CC sequence is human RET16.2 splice variant DNA
XX
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DB 181 TCTTGGTACTTGTCTCTTGGACAAACCAATTCGCTGTAAGTCTTCTTCTTCC 240
QY 241 AACTGCACATTCCTCATTAAGTTTCACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 AACTGCACATTCCTCATTAAGTTTCACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CTTTCAAGACATATTTTGGCATTCGTTTCAACAGATGCTACCTGCTTATGGAATCTG 360
DB 301 CTTTCAAGACATATTTTGGCATTCGTTTCAACAGATGCTACCTGCTTATGGAATCTG 360
QY 361 AAAATGACAGATGCTGCGAGTATGGAACGCTTAAGTGGACCGCTGTAGAGGTTTGGC 420
DB 361 AAAATGACAGATGCTGCGAGTATGGAACGCTTAAGTGGACCGCTGTAGAGGTTTGGC 420
QY 421 AGTTTTCCCGAGACTCAGCTGTTTGGCATCAGGGGAGCTGATGGAATCTGCTTGT 480
DB 421 AGTTTTCCCGAGACTCAGCTGTTTGGCATCAGGGGAGCTGATGGAATCTGCTTGT 480
QY 481 GGAATGACAGTCAATCAAAATTAATATAGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GGAATGACAGTCAATCAAAATTAATATAGATGATGATGATGATGATGATGATGATGAT 540
QY 541 CATGTGATTTTCTTCCCTAATGGAAGCTTCTTGGCATGCTGCTCTCTCATGTGATTTAA 600
DB 541 CATGTGATTTTCTTCCCTAATGGAAGCTTCTTGGCATGCTGCTCTCTCATGTGATTTAA 600

QY 601 CAGTGTGGATGATTAATAATGAGGTGCTGCTGATGATGATGATGATGATGATGATGATGAT 660
DB 601 CAGTGTGGATGATTAATAATGAGGTGCTGCTGATGATGATGATGATGATGATGATGATGAT 660
QY 661 CCGTGTGGATTTTCTTCAACAGCCAGTTTCTGATGAGAAACAGGTCTTCAAGTTTTC 720
DB 661 CCGTGTGGATTTTCTTCAACAGCCAGTTTCTGATGAGAAACAGGTCTTCAAGTTTTC 720
QY 721 GACTGCATCATGTTGCTGAGTATGCGAAGTCAAAATTTGATGTTTCTTTTACCAAT 780
DB 721 GACTGCATCATGTTGCTGAGTATGCGAAGTCAAAATTTGATGTTTCTTTTACCAAT 780
QY 781 TCTTACCAAGCGCAGACAGAACATCAGCTGAAGCAATTTCCGAAGTTGCTGAGAGG 840
DB 781 TCTTACCAAGCGCAGACAGAACATCAGCTGAAGCAATTTCCGAAGTTGCTGAGAGG 840
QY 841 TCGTCTCAACATGCTTTTGTGCAACAGATTTAAAGATCTTGTGATTTTCAAGATGA 900
DB 841 TCGTCTCAACATGCTTTTGTGCAACAGATTTAAAGATCTTGTGATTTTCAAGATGA 900
QY 901 ATTAACATTTGATGAAAAAGAACTGTTGATCTTCAAAAGAAAGTCTGCTGATGATTTGA 960
DB 901 ATTAACATTTGATGAAAAAGAACTGTTGATCTTCAAAAGAAAGTCTGCTGATGATTTGA 960
QY 961 AAATTAATCTCTAGAGCTGCGTATGAAAGTGTGAGAAATTTGAAGAGCTCAGAGCA 1020
DB 961 AAATTAATCTCTAGAGCTGCGTATGAAAGTGTGAGAAATTTGAAGAGCTCAGAGCA 1020
QY 1021 AGGTAAATCTCTTCTTCAAGAAATCTGATGAAATTTATATGCTCAATPACTAGAAAC 1080
DB 1021 AGGTAAATCTCTTCTTCAAGAAATCTGATGAAATTTATATGCTCAATPACTAGAAAC 1080
QY 1081 TTAATGAAAGATCCGGTCAATGCGATGATGCGATTCATATGATGAAAGAAAGCAATGAAA 1140
DB 1081 TTAATGAAAGATCCGGTCAATGCGATGATGCGATTCATATGATGAAAGAAAGCAATGAAA 1140
QY 1141 ATTGATCAGCAAAAAGAAACGTACAGTCCCATGCAATCTTGTCTTCTTCAAGCG 1200
DB 1141 ATTGATCAGCAAAAAGAAACGTACAGTCCCATGCAATCTTGTCTTCTTCAAGCG 1200
QY 1201 TACTTACACCAATATAGACTCTGAAAATGCGCATATATGATGCTGAGACACACCA 1260
DB 1201 TACTTACACCAATATAGACTCTGAAAATGCGCATATATGATGCTGAGACACACCA 1260
QY 1261 AGTAAAGAAATTC 1272
DB 1261 AGTAAAGAAATTC 1272
RESULT 2
AAD45071
ID AAD45071 standard; DNA; 1553 BP.
XX
AC AAD45071;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human RET16 open reading frame (ORF) DNA.
XX
XX Human; RET16; intracellular signal; inflammation-related disease; asthma;
XX rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
XX transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
XX inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
XX inacute respiratory distress syndrome; cardiac; ulcerative colitis;
XX autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
XX cellular migration disorder; cell proliferation disorder; calcification;
XX hyperinsulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
XX cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
XX thalassaemia; vasotropic; open reading frame; ORF; gene; ds.
XX
OS Homo sapiens.
XX

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FH Key Location/Qualifiers
FT CDS 3..1541
FT /tag= a
FT /product= "Human RET16 protein"
FT /note= "CDS does not include start codon"
FT /partial
XX MO200266494-A2.
XX
XX 29-AUG-2002.
XX
XX 15-FEB-2002; 2002MO-US005162.
XX PF
XX 16-FEB-2001; 2001US-0269366P.
XX PR
XX 29-MAY-2001; 2001US-0294181P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Todderud CG, Finger JN, Rillema J;
XX
XX WPI; 2002-682760/73.
XX DR
XX P-PSDB; AAE28164.
XX
XX New human, mouse or rat RET16 genes and proteins, involved in
XX intracellular signaling cascade, useful for in gene therapy, particularly
XX for treating e.g. ischemia, cystic fibrosis, autoimmune disease, cancers,
XX tumors or neoplasms.
XX
XX Claim 1; Page 150; 175pp; English.
XX
XX The invention relates to human, mouse or rat RET16 genes and proteins,
XX involved in intracellular signaling cascade. The RET16 protein or
XX polynucleotide is useful for treating an inflammation-related disease or
XX disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
XX asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
XX tissue transplants, chronic obstructive pulmonary disease, inflammatory
XX bowel disease, Crohn's disease, ulcerative colitis, inacute respiratory
XX distress syndrome, systemic lupus erythematosus, autoimmune disease,
XX cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
XX disease or disorder also includes disorders associated with aberrant
XX activation of the TNF-alpha pathway, disorders associated with aberrant
XX cellular migration, proliferation, metastasis, juvenile idiopathic
XX arthritis, haematogenous metastases of tumour cells, hyperinsulinaemia,
XX diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
XX tumour progression, Wegener's granulomatosis, stem cell transplantation
XX complications, ischaemia-reperfusion injury, thalassemia, acute lung
XX injury, graft rejection, ischaemic heart, coronary artery calcification
XX or allergic inflammation. RET16 DNA is used in gene therapy. The present
XX sequence is human RET16 open reading frame (ORF) DNA
XX
XX
XX Sequence 1553 BP; 428 A; 327 C; 348 G; 450 T; 0 U; 0 Other;
XX
XX Query Match 76.8%; Score 977.2; DB 6; Length 1553;
XX Best Local Similarity 81.9%; Pred. No. 4.9e-288;
XX Matches 1265; Conservative 0; Mismatches 3; Indels 276; Gaps 1;
XX
XX
XX 1 GAATTCGGCTTTTCACTCGCGGACGTCGACCCGCGGCGGACCTTTGAAGCG 60
XX 1 GAATTCGGCTTTTCACTCGCGGACGTCGACCCGCGGCGGACCTTTGAAGCG 60
XX
XX 61 GATCCCGCGGCGCGCGCTCTCGAGGCTGTTTCTTCAATTAAGAACTGGTGAAC 120
XX 61 GATCCCGCGGCGCGCGCTCTCGAGGCTGTTTCTTCAATTAAGAACTGGTGAAC 120
XX
XX 121 TGATTCACATTAAGTCATCATGTGACATGTCACACTGCTGCTTCTTCC 180
XX 121 TGATTCACATTAAGTCATCATGTGACATGTCACACTGCTGCTTCTTCC 180
XX
XX 181 TCTTGGCTACTGCTGCTTGGACAAACAAATTCGCTGCTGCTGCTGCTTACTG 240
XX 181 TCTTGGCTACTGCTGCTTGGACAAACAAATTCGCTGCTGCTGCTGCTTACTG 240
XX
XX 241 AACTGCCACATTTCCATGTAAGTTTCACTATGCTGCTGCTGCTGCTTCTCC 300

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Db 241 AACTGCCACATTTCCATGTAAGTTTCACTATGCTGCTGCTGCTGCTTCTCC 300
Qy 301 CTTGAGCAGATATTTTGGCATGCTGTTCAACAGATGTTACCATGCTTATGGAATCTG 360
Db 301 CTTGAGCAGATATTTTGGCATGCTGTTCAACAGATGTTACCATGCTTATGGAATCTG 360
Qy 361 AAAATGACAGATGCTGCGAGTATGGAACAGCTGTGAGCGCCGTGAGGCTTGCC 420
Db 361 AAAATGACAGATGCTGCGAGTATGGAACAGCTGTGAGCGCCGTGAGGCTTGCC 420
Qy 421 AGTTTTCGCCAGATCCACGCTGTTTGGCATCAGGCGCAGCTGATGGAACCTGCTTGT 480
Db 421 AGTTTTCGCCAGATCCACGCTGTTTGGCATCAGGCGCAGCTGATGGAACCTGCTTGT 480
Qy 481 GGAATGACAGTATACAAATTTATATGATGCTGCTGTTAAAGATGCTCTTGGCGG 540
Db 481 GGAATGACAGTATACAAATTTATATGATGCTGCTGTTAAAGATGCTCTTGGCGG 540
Qy 541 CATGTGATTTTCTCTCAATGGAAGCTTCTTGTCACTGCTCCTCATGTTGATTTAA 600
Db 541 CATGTGATTTTCTCTCAATGGAAGCTTCTTGTCACTGCTCCTCATGTTGATTTAA 600
Qy 601 CAGTGTGGATGATTAATAATGAGTGTCTGATAGTGAATAAGACATGATCTTGAATTA 660
Db 601 CAGTGTGGATGATTAATAATGAGTGTCTGATAGTGAATAAGACATGATCTTGAATTA 660
Qy 661 CTGTGCTGCAATTTTCTTCAACAGCAGTCTGTATGAGAAACAAGTCTTCACTTTTTC 720
Db 661 CTGTGCTGCAATTTTCTTCAACAGCAGTCTGTATGAGAAACAAGTCTTCACTTTTTC 720
Qy 721 GACTGGCATATGTCGTCAGATTTGCCAAGTCAAAATTTGATGTTCTTTTACCATA 780
Db 721 GACTGGCATATGTCGTCAGATTTGCCAAGTCAAAATTTGATGTTCTTTTACCATA 780
Qy 781 TCTTAGTTTGAATTAATAATTAAGTACACTGAGTGGCACTGCTCCTGTTCTGG 840
Db 781 TCTTAGTTTGAATTAATAATTAAGTACACTGAGTGGCACTGCTCCTGTTCTGG 840
Qy 785 ----- 784
Db 785 ----- 784
Qy 841 CTTGTGCTTTTCCCGATGAGCAGATGTCAGTCTCAGGCTGATGATTAAGTCTGCA 900
Db 841 CTTGTGCTTTTCCCGATGAGCAGATGTCAGTCTCAGGCTGATGATTAAGTCTGCA 900
Qy 785 ----- 784
Db 785 ----- 784
Qy 901 TAGATATGATTAATTAATGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Db 901 TAGATATGATTAATTAATGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Qy 785 ----- 784
Db 785 ----- 784
Qy 961 TCACAACTTGCTTTTGAACCTAATACCTTTTACTTGTGCTGCTTCAATGACAAA 1020
Db 961 TCACAACTTGCTTTTGAACCTAATACCTTTTACTTGTGCTGCTTCAATGACAAA 1020
Qy 785 ----- 784
Db 785 ----- 784
Qy 1021 CAGTGAACATCTGGCAATTTGACCTGGAACACCTTTGCCAAGCAAGCGGACGAAACATC 1080
Db 1021 CAGTGAACATCTGGCAATTTGACCTGGAACACCTTTGCCAAGCAAGCGGACGAAACATC 1080
Qy 805 AGCTGAAGCAATTTTACCGAAGATTTGTCAGAGAGTGTCTCAACATGCTTGTGCAC 864
Db 805 AGCTGAAGCAATTTTACCGAAGATTTGTCAGAGAGTGTCTCAACATGCTTGTGCAC 864
Qy 1081 AGCTGAAGCAATTTTACCGAAGATTTGTCAGAGAGTGTCTCAACATGCTTGTGCAC 1140
Db 1081 AGCTGAAGCAATTTTACCGAAGATTTGTCAGAGAGTGTCTCAACATGCTTGTGCAC 1140
Qy 865 AAGATTTAAAGATCTTGTGTTATTTTCAAGATGAATTAATTAATTAATTAATTAAT 924
Db 865 AAGATTTAAAGATCTTGTGTTATTTTCAAGATGAATTAATTAATTAATTAATTAAT 924
Qy 1141 AAGATTTAAAGATCTTGTGTTATTTTCAAGATGAATTAATTAATTAATTAATTAAT 1200
Db 1141 AAGATTTAAAGATCTTGTGTTATTTTCAAGATGAATTAATTAATTAATTAATTAAT 1200
Qy 925 TGAATCTTAACAAAGAAAGTCTGCTGATGATTTGAATAATTAATTAATTAATTAAT 984
Db 925 TGAATCTTAACAAAGAAAGTCTGCTGATGATTTGAATAATTAATTAATTAATTAAT 984
Qy 985 GTAAGTGTGAGGAAATTAAGAGCTCAGAGCAAGTAAATCCCTTTCTTCAAGAA 1044
Db 985 GTAAGTGTGAGGAAATTAAGAGCTCAGAGCAAGTAAATCCCTTTCTTCAAGAA 1044
Qy 1261 GTAAGTGTGAGGAAATTAAGAGCTCAGAGCAAGTAAATCCCTTTCTTCAAGAA 1320
Db 1261 GTAAGTGTGAGGAAATTAAGAGCTCAGAGCAAGTAAATCCCTTTCTTCAAGAA 1320
Qy 1045 TTCTGATGAATTTATATGTCATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1104
Db 1045 TTCTGATGAATTTATATGTCATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1104

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Db      589 TCTCCTAATGGAAGCTTCTTTGTCACTGGCTCCTCATGTCGTGATTTAAACAGTGTGGAT 648
QY      612 GATAAATAGGAGTGTGCACTAGTAAAAAGCAGATCTTGGAAATACCTGCTCGAT 671
Db      649 GATAAATAGGAGTGTGCACTAGTAAAAAGCAGATCTTGGAAATACCTGCTCGAT 708
QY      672 TTTTCTTCAAGCAGCTTTCTGTAGAGAAACAGGCTTTCAGTTTTCAGCTGCGATCA 731
Db      709 TTTTCTTCAAGCAGCTTTCTGTAGAGAAACAGGCTTTCAGTTTTCAGCTGCGATCA 768
QY      732 TGTGTGACAGATTGCCAAGTCAAAATTTGGATGTTTCTTTTACCCATATCTT----- 784
Db      769 TGTGTGACAGATTGCCAAGTCAAAATTTGGATGTTTCTTTTACCCATATCTTGGATTT 828
QY      785 ----- 784
Db      829 GAATTAATAATAAAATACACTGAGTGGGCACTGTCTCTGCTTGTGCTTGT 888
QY      785 ----- 784
Db      889 TCCCATGATGGGAGATGCTAGTCTCAGGGTCAAGGATTAAGTCTGTCAATATATGAT 948
QY      785 ----- 784
Db      949 ACTAATACTGAGAATATACTTACACATTGACTCAGACACACAGATATGTCAACAATTGT 1008
QY      785 ----- 784
Db      1009 GCTTTTGACCTAATATCCCTTTTACTTGTCTACTGTTCATATGACAAACAGTGAACATC 1068
QY      785 -----AGCAAGGCGCACAGACATCAGCTGAAGCAA 815
Db      1069 TGGCAATTTGACCTGGAAACACTTTGGCAAGCAAGAGACACAGAACTCAGCTGAAGCAA 1128
QY      816 TTTTCCGAAGATTGGTCAAGAGAGTGTCTCAACATGCTTGTGTGACAAAGTTTAAAA 875
Db      1129 TTTTCCGAAGATTGGTCAAGAGAGTGTCTCAACATGCTTGTGTGACAAAGTTTAAAA 1188
QY      876 GATCTTGTGTGATTTTTCAGATGAATTAACATTGATGAAAGAAAGAACTGTGAATCTTACA 935
Db      1189 GATCTTGTGTGATTTTTCAGATGAATTAACATTGATGAAAGAAAGAACTGTGAATCTTACA 1248
QY      936 AAGAAAGTCTGCTGATGATTTGAAAATTGAAATCTTCAAGACTGCGTAAAGTCTG 995
Db      1249 AAGAAAGTCTGCTGATGATTTGAAAATTGAAATCTTCAAGACTGCGTAAAGTCTG 1308
QY      996 AGAAATTTGAAGAGCTCAGAGACCAAGTTAAATCCCTTCTCAGAAATTCCTGATGAA 1055
Db      1309 AGAAATTTGAAGAGCTCAGAGACCAAGTTAAATCCCTTCTCAGAAATTCCTGATGAA 1368
QY      1056 TTTATATGTCGAATTAAGAGAACTTAAGAAAGTCCGTCATCGCATCAGATGGCTAT 1115
Db      1369 TTTATATGTCGAATTAAGAGAACTTAAGAAAGTCCGTCATCGCATCAGATGGCTAT 1428
QY      1116 TCATATGAAAAGAGCAATGAAAATTGGATAGCAAAAAAGAAACGTACAACTCCCATG 1175
Db      1429 TCATATGAAAAGAGCAATGAAAATTGGATAGCAAAAAAGAAACGTACAACTCCCATG 1488
QY      1176 ACAAAATCTTGTCTTCTTCTCAGGGTACTTACACCAAAATAGAGCTGTGAAAATGGGCATC 1235
Db      1489 ACAAAATCTTGTCTTCTTCTCAGGGTACTTACACCAAAATAGAGCTGTGAAAATGGGCATC 1548
QY      1236 AATAGATGGCTGAGACACACCAAAAGTAAA 1266
Db      1549 AATAGATGGCTGAGACACACCAAAAGTAAA 1579

RESULT 5
AA158876
ID      AA158876 standard; cdNA; 1844 BP.
XX
AC
XX      AA158876;
XX
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DT      22-OCT-2001 (first entry)
XX
XX      Human polynucleotide SEQ ID NO 1079.
DE
XX      Human; nootropic; immunosuppressant; cytotactic; gene therapy; cancer;
KW      peripheral nervous system; neuropathy; central nervous system; CNS;
KW      Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW      amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW      chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW      leukemia; ss.
XX
OS      Homo sapiens.
XX
PN      WO200153312-A1.
XX
PD      26-JUL-2001.
XX
PF      26-DEC-2000; 2000WO-US034263.
XX
PR      23-DEC-1999; 99US-00471275.
PR      21-JAN-2000; 2000US-00488725.
PR      25-APR-2000; 2000US-00552317.
PR      20-JUN-2000; 2000US-00598042.
PR      19-JUL-2000; 2000US-00620312.
PR      03-AUG-2000; 2000US-00653450.
PR      14-SEP-2000; 2000US-00662191.
PR      19-OCT-2000; 2000US-00693036.
PR      29-NOV-2000; 2000US-00727344.
XX
PA      (HYSE-) HYSEQ INC.
PI      Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI      Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI      Zhou P, Goodrich R, Dermanic RT;
XX
DR      WPI; 2001-442253/47.
DR      P-PSDB; AAM39720.
XX
PT      Novel nucleic acids and polypeptides, useful for treating disorders such
PT      as central nervous system injuries.
XX
PS      Claim 1; SEQ ID NO 1079; 10078bp; English.
XX
XX      The invention relates to human nucleic acids (AA157798-AA161369) and the
XX      encoded polypeptides (AA138642-AA42213) with nootropic,
XX      immunosuppressant and cytosaric activity. The polynucleotides are useful
XX      in gene therapy. A composition containing a polypeptide or polynucleotide
XX      of the invention may be used to treat diseases of the peripheral nervous
XX      system, such as peripheral nervous injuries, peripheral neuropathy and
XX      localized neuropathies and central nervous system diseases, such as
XX      Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX      lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX      utilisation of the activities such as: Immune system suppression,
XX      Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX      and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX      assays for receptor activity, arthritis and inflammation, leukemias and
XX      C.N.S disorders. Note: The sequence data for this patent did not form
XX      part of the printed specification
XX
SQ      Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other:
XX

Query Match      75.8%; Score 964.2; DB 4; Length 1844;
Best Local Similarity 81.8%; Pred. No. 5.2e-284;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY      12 TCACCTGCGCGCAGCTGACCCGACCGCCGCTGGGACCTTGAAGCGCGATCCCGCGG 71
Db      65 TCACCTGCGCGCAGCTGACCCGACCGCCGCTGGGACCTTGAAGCGCGATCCCGCGG 124
QY      72 CCCCCGCTCTGACAGGCTGTTTCTTCAATTAAGAAACATGATGTAATTCATCACA 131
Db      125 CCCCCGCTCTGACAGGCTGTTTCTTCAATTAAGAAACATGATGTAATTCATCACA 184
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Oy	132	TTAGCTGATCAATGGGAGAGATGTCAACTGCTGTGCTCTCTCTTTCCCTCTTGCTACT	191
Db	185	TTAGCTGATCAATGGGAGAGATGTCAACTGCTGTGCTCTCTCTTTCCCTCTTGCTACT	244
Oy	192	TGCTCTCTGGACAAAACAATTGCGCTGTACTGCTTAACGTGACCTTAACGTGACCAT	251
Db	245	TGCTCTCTGGACAAAACAATTGCGCTGTACTGCTTAACGTGACCTTAACGTGACCAT	304
Oy	252	TCTCCATTGAAGTTTCATACCTTAATGCTGTGCACTGCTGCTGTTTCTCCCTTCAGACAT	311
Db	305	TCTCCATTGAAGTTTCATACCTTAATGCTGTGCACTGCTGCTGTTTCTCCCTTCAGACAT	364
Oy	312	ATTTTGGATGCTGTTCAACAGATGCTGTAACACTGTCTCTTAATGGAATACGTGAAATGACAG	371
Db	365	ATTTTGGATGCTGTTCAACAGATGCTGTAACACTGTCTCTTAATGGAATACGTGAAATGACAG	424
Oy	372	ATGCTGGAGATGATGAGAACAGCTCTAGTGGACGCGCTGTAGGGCTTTGCGAGTTTCCCA	431
Db	425	ATGCTGGAGATGATGAGAACAGCTCTAGTGGACGCGCTGTAGGGCTTTGCGAGTTTCCCA	484
Oy	432	GACTCCACGTGTTTGGCATACAGGGGACGCTGATGGAACGTGTGTTTGTGGAATGACAG	491
Db	485	GACTCCACGTGTTTGGCATACAGGGGACGCTGATGGAACGTGTGTTTGTGGAATGACAG	544
Oy	492	TCATACAAATATATAGATGTGTGTGATGTGTTAAAGATGCGCTCTTGCGCGACATGTCATTT	551
Db	545	TCATACAAATATATAGATGTGTGTGATGTGTTAAAGATGCGCTCTTGCGCGACATGTCATTT	604
Oy	552	TCTCCTAATGGAAGCTTCTTTGTGCACTGCGCTCATATGGGATTTTAAACGTGTGGAT	611
Db	605	TCTCCTAATGGAAGCTTCTTTGTGCACTGCGCTCATATGGGATTTTAAACGTGTGGAT	664
Oy	612	GATAAAATGAGGTGTCTGCATAGTAAAAAGACACATGATCTTTGGAATTAACGTGCGCAT	671
Db	665	GATAAAATGAGGTGTCTGCATAGTAAAAAGACACATGATCTTTGGAATTAACGTGCGCAT	724
Oy	672	TTTTCTTCAACGCGATTTCTGTAGTGGAGAACAGGTCTTCAGTTTCTTTCGACTGSCATCA	731
Db	725	TTTTCTTCAACGCGATTTCTGTAGTGGAGAACAGGTCTTCAGTTTCTTTCGACTGSCATCA	784
Oy	732	TGTGTGATGAGATTGCCAAGTCAAAATTTTGGATTTGTTCTTTTACCCTATATCTT-----	784
Db	785	TGTGTGATGAGATTGCCAAGTCAAAATTTTGGATTTGTTCTTTTACCCTATATCTT-----	844
Oy	785	-----	784
Db	845	GAATTTAAATATATAAAGTACACTGAGTGGGACACTGTGCTCCGTGTTCTGCTGTGTGCTTTT	904
Oy	785	-----	784
Db	905	TCCCATGATGGGACAGATGCTAGTCTCAGGGTCAGTGATTAAGTCTGTCAATAGTATATGAT	964
Oy	785	-----	784
Db	965	ACTAATACTGAGAAATATACTTCACACATTGACTCAGACACACGAGTATGTACAACTTGT	1024
Oy	785	-----	784
Db	1025	GCTTTTGCACCTAATAACCTTTTACTTGCTACTGTTCAATGACAAAACAGTGAACATC	1084
Oy	785	-----AGCAAGCGCACAGAACATCAGCTGAAGCA	815
Db	1085	TGGCAATTTTGAACCTGGAACAACCTTTGCCAAGCAAGAGACAGAACATCAGCTGAAGCA	1144
Oy	816	TTTACCAGGAAGTTGGTCAAGAGAGTCTGTCAACATGGCTTTTGTGCACAGATTTTAA	875
Db	1145	TTTACCAGGAAGTTGGTCAAGAGAGTCTGTCAACATGGCTTTTGTGCACAGATTTTAA	1204
Oy	876	GATCTGTGTTGTAATTTTCAAGATGGAATACATTTGATGAAAAAGACTGTGTAATCTTACA	935
Db	1205	GATCTGTGTTGTAATTTTCAAGATGGAATACATTTGATGAAAAAGACTGTGTAATCTTACA	1264
Oy	936	AAAGAAAGTCTGGCTGATGATTTGAAAATTTGAATCTTAAGACTGCGTAAAGTGTCTG	995

Dd	1265	AAAGAAAGCTCGCTGATGATTTTGAATACTTAGAGACTGCTAGTAAAGTCTG	1324
Qy	996	AGGAAATTTGMAAGCTCAGAGCCAGGTTAAATCCCTTTCTTGAGAAATTCGTATGAA	1055
Dd	1325	AGGAAATTTGMAAGCTCAGAGCCAGGTTAAATCCCTTTCTTGAGAAATTCGTATGAA	1384
Qy	1056	TTTATATGTCCTAATPACTAGAGAACTTATGAAAGATCCGGTCATCGCATCGATGCTAT	1115
Dd	1385	TTTATATGTCCTAATPACTAGAGAACTTATGAAAGATCCGGTCATCGCATCGATGCTAT	1444
Qy	1116	TCATATGAAAAAGGAAGCAATGAAAAATTTGGATCGCAAAAAAGAAACGTAAGTCCCATG	1175
Dd	1445	TCATATGAAAAAGGAAGCAATGAAAAATTTGGATCGCAAAAAAGAAACGTAAGTCCCATG	1504
Qy	1176	ACAAATCTTGTCTCTTCCTTCAGCGGTACTTACACCAATAGAGACTGTGAAAAATGGCCATC	1233
Dd	1505	ACAAATCTTGTCTCTTCCTTCAGCGGTACTTACACCAATAGAGACTGTGAAAAATGGCCATC	1564
Qy	1236	AATAGATGCTGAGACACACCAAAAAAGTAA	1266
Dd	1565	AATAGATGCTGAGACACACCAAAAAAGTAA	1595
RESULT 6			
ADQ99098	ID	ADQ99098 standard; cDNA; 1844 BP.	
AC	ADQ99098;		
DT	23-SEP-2004	(first entry)	
DE	DNA encoding human GPCR-like protein seqid 768.		
KM	ophthalmological; immunomodulatory; cystostatic; antiatherosclerotic;		
KM	antidiabetic; GPCR-like protein; ophthalmic disorder;		
KM	neurological disorder; immunological disorder; nephritic disorder;		
KM	hormonal dysfunction; cancer; atherosclerosis; diabetes;		
XX	molecular weight marker; food supplement; human; ss.		
OS	Homo sapiens.		
PN	US6569662-B1.		
PD	27-MAY-2003.		
PF	19-JUL-2000; 2000US-00620312.		
PR	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00552317.		
PA	(HYSE-) HYSEQ INC.		
XX	Tang YT, Zhou P, Drmanac RT;		
XX	WPI; 2001-442255/47.		
XX	New G-Protein-coupled receptor-like polypeptides and polynucleotides,		
XX	useful for treating diseases of ophthalmic, neurological, immunological		
XX	and nephritic systems and hormonal dysfunction, cancer, atherosclerosis		
XX	and diabetes.		
XX	Example 2; SEQ ID NO 768; 92pp; English.		
XX	The invention describes an isolated polynucleotide (I) comprising a fully		
XX	defined (51) OF 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041,		
XX	1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as		
XX	given in the specification, its translated or protein coding portion, its		
XX	extracellular portion or its active domain. The GPCR-like polypeptides		
XX	and polynucleotides are useful for the treatment of diseases of		
XX	ophthalmic, neurological, immunological and nephritic systems. They may		
XX	be used to treat hormonal dysfunction, cancer, atherosclerosis and		
XX	diabetes. The antibodies are useful for detecting or quantitating the		

CC polypeptide in tissue. The polypeptides can also be used as molecular
 CC weight markers and as a food supplement. This sequence represents a human
 CC polynucleotide of the invention.

XX Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other;

Query Match 75.8%; Score 964.2; DB 5; Length 1844;
 Best Local Similarity 81.8%; Pred. No. 5.2e-284;
 Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

```

QY 12 TCACCTGCGGGGACGTCGACCCGACCCCGGGGACCTTGAAGCGGATCCCGCG 71
DB 65 TCACCTGCGGGGACGTCGACCCGACCCCGGGGACCTTGAAGCGGATCCCGCG 124
QY 72 CCCCCCTCCTGACGCGTCTTTCTTCAATAAAGAACATGGGAAACGATTTCACAC 131
DB 125 CCCCCCTCCTGACGCGTCTTTCTTCAATAAAGAACATGGGAAACGATTTCACAC 184
QY 132 TTAGCTGATCAGTGAAGATGTCACCTGCTGCTCTCTCTCTCTCTCTCTCTCT 191
DB 185 TTAGCTGATCAGTGAAGATGTCACCTGCTGCTCTCTCTCTCTCTCTCTCTCT 244
QY 192 TGGTCTTGGACAAACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 251
DB 245 TGGTCTTGGACAAACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
QY 252 TCTCCATTGAAGTTGATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
DB 305 TCTCCATTGAAGTTGATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
QY 312 ATTTGGCATGCTGTTCAACAGATGTCACCTGCTGCTGCTGCTGCTGCTGCTG 371
DB 365 ATTTGGCATGCTGTTCAACAGATGTCACCTGCTGCTGCTGCTGCTGCTGCTG 424
QY 372 ATGCTGGCAGTGAAGACGCTGAGGACGCTGAGGCTGAGGCTGAGGCTGAGG 431
DB 425 ATGCTGGCAGTGAAGACGCTGAGGACGCTGAGGCTGAGGCTGAGGCTGAGG 484
QY 432 GACTCCACGTTTGGCATCAGGGGACGTCGATGAACTGTGTTTGTGGAATGCA 491
DB 485 GACTCCACGTTTGGCATCAGGGGACGTCGATGAACTGTGTTTGTGGAATGCA 544
QY 492 TCATCAAAATTATATAGATGTGATGTTTAAAGATGCTCTTGGCGGATGCA 551
DB 545 TCATCAAAATTATATAGATGTGATGTTTAAAGATGCTCTTGGCGGATGCA 604
QY 552 TCTCCCTAAATGAGAGCTCTTCTTGTACAGGCTCTCTCAATGTGTGATTTAA 611
DB 605 TCTCCCTAAATGAGAGCTCTTCTTGTACAGGCTCTCTCAATGTGTGATTTAA 664
QY 612 GATAAATGAGAGTGTCTGATAGTGAAGAACATGATCTTGAATTAACCTGCG 671
DB 665 GATAAATGAGAGTGTCTGATAGTGAAGAACATGATCTTGAATTAACCTGCG 724
QY 672 TTTTCTTCAACGCAAGTTTCTGATGAGAACAGAGTCTTCAAGTTTTCAG 731
DB 725 TTTTCTTCAACGCAAGTTTCTGATGAGAACAGAGTCTTCAAGTTTTCAG 784
QY 732 TGTGGTCAGGATGGCAAGTCAAAATTTGATGTTTCTTTTACCAATATCT 784
DB 785 TGTGGTCAGGATGGCAAGTCAAAATTTGATGTTTCTTTTACCAATATCT 844
QY 785 ----- 784
DB 845 GAATTAATAATATAAGTACACTGAGTGGGACGTCGCTCTGTTCTGCGCTT 904
QY 785 ----- 784
DB 905 TCCCATGATGGGACGATGCTAGTCTCAGGGTCAGTGAATAGTCTGTCATATAT 964
QY 785 ----- 784
DB 965 ACTAATACGAGAAATATCTTCAACATTTGATCAGACACCAAGTATGTCAAC 1024

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QY 785 ----- 784
DB 1025 GCTTTTGACCTAATACCTTTTACTGTCTGTTCAATGACAAAACAGTGAAC 1084
QY 785 ----- AGAAGCGGACAGAACATCAGTGAACAA 815
DB 1085 TGSCAATTTGACCTGGAACACTTTGCCAAGCAAGGACAGAACATCAGCTGA 1144
QY 816 TTTTACCGAAGATTGGTCAGAGAGGTCGTCGAACATGCTTTGTGACAAAGTT 875
DB 1145 TTTTACCGAAGATTGGTCAGAGAGGTCGTCGAACATGCTTTGTGACAAAG 1204
QY 876 GATCTTGTGTAATTTTCAAGATGAATACATTTGATGAAAAAGAACTGTGAAT 935
DB 1205 GATCTTGTGTAATTTTCAAGATGAATACATTTGATGAAAAAGAACTGTGAAT 1264
QY 936 AAGAAAGTCTGCTGATGATTTGAAAATGGAATCTTAGACCTGCTGTAAGT 995
DB 1265 AAGAAAGTCTGCTGATGATTTGAAAATGGAATCTTAGACCTGCTGTAAGT 1324
QY 996 AAGAAATTTGAAGAGCTCAGACCAAGTTAAATCCCTTTCAAGAAATCCTG 1055
DB 1325 AAGAAATTTGAAGAGCTCAGACCAAGTTAAATCCCTTTCAAGAAATCCTG 1384
QY 1056 TTTATATGTCAAATACTAGAGAACTTATGAAAAGATCCGTCATCGCATG 1115
DB 1385 TTTATATGTCAAATACTAGAGAACTTATGAAAAGATCCGTCATCGCATG 1444
QY 1116 TCTATGAAAAGGACCAATGGAATTTGATCAGAAAAAGAACGTCAAGTCC 1175
DB 1445 TCTATGAAAAGGACCAATGGAATTTGATCAGAAAAAGAACGTCAAGTCC 1504
QY 1176 ACAATCTTGTCTTCTTCAAGCGTACTTACACCAATAGGACTGTGAATG 1235
DB 1505 ACAATCTTGTCTTCTTCAAGCGTACTTACACCAATAGGACTGTGAATG 1564
QY 1236 AATGATGCTGAGACACACCAAAAAGTAAA 1266
DB 1565 AATGATGCTGAGACACACCAAAAAGTAAA 1595

RESULT 7
ADB48858
ID ADB48858 standard; cDNA; 1844 BP.
XX
AC ADB48858;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA SEQ ID NO 768.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PF 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIU/) LIU C.
PA (ASUNDI/) ASUNDI V.
PA (DRMANAC/) DRMANAC R T.
XX
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;

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XX WPI; 2003-678194/64.
 DR New polynucleotide, useful for treating diseases e.g., cancer or
 PT neurodegenerative diseases.
 XX
 PS Claim 1; SEQ ID NO 768; 99p; English.
 XX
 CC The invention relates to a polynucleotide comprising a sequence given in
 CC the specification, or its mature protein-coding portion, or its
 CC complement. The polynucleotide is useful for treating diseases e.g.,
 CC cancer or neurodegenerative diseases and many others listed in the
 CC specification. The present sequence represents a novel human cDNA. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPRO
 CC at seqdata.uspro.gov/sequence.html?docID=20030104529.
 XX
 XX Sequence 1844 BP; 535 A; 380 C; 389 G; 540 T; 0 U; 0 Other;
 Query Match 75.8%; Score 964.2; DB 9; Length 1844;
 Best Local Similarity 81.8%; Pred. No. 5.2e-284;
 Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;
 QY 12 TCACTGCGCGGACGTCGACCCGACCCCGTGGGACCTTGAAGCGGATCCCGCG 71
 DB 65 TCACTGCGCGGACGTCGACCCGACCCCGTGGGACCTTGAAGCGGATCCCGCG 124
 QY 72 CCCCCCTCTCGACGCTGTTTTCTTCAATAAAGACATGTAAGTATTCACACA 131
 DB 125 CCCCCCTCTCGACGCTGTTTTCTTCAATAAAGACATGTAAGTATTCACACA 184
 QY 132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
 DB 185 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244
 QY 192 TGTCTCTTGACAAACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
 DB 245 TGTCTCTTGACAAACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
 QY 252 TGTCTCTTGACAAACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
 DB 305 TGTCTCTTGACAAACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
 QY 312 ATTTGGCATCGTGTAAACAGATGTAACAGATGTAACAGATGTAACAGATGTA 371
 DB 365 ATTTGGCATCGTGTAAACAGATGTAACAGATGTAACAGATGTAACAGATGTA 424
 QY 372 ATGCTGCAATGATGTAACAGATGTAACAGATGTAACAGATGTAACAGATGTA 431
 DB 425 ATGCTGCAATGATGTAACAGATGTAACAGATGTAACAGATGTAACAGATGTA 484
 QY 432 GACTCCAGTGTGTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 491
 DB 485 GACTCCAGTGTGTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 544
 QY 492 TCATACAAATTAATTAATGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 551
 DB 545 TCATACAAATTAATTAATGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 604
 QY 552 TCTCTTAATGAGAGCTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
 DB 605 TCTCTTAATGAGAGCTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 664
 QY 612 GATTAATGAGAGTGTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 671
 DB 665 GATTAATGAGAGTGTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 724
 QY 672 TTTTCTTCAAGCAGTTTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 731
 DB 725 TTTTCTTCAAGCAGTTTCTGATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 784
 QY 732 TGTGTCAGAGATTGCCAAGTCMAAATTTGATTTTCTTTTACCAATCTT----- 784

DB 785 TGTGTCAGAGATTGCCAAGTCMAAATTTGATTTTCTTTTACCAATCTTAGTTTT 844
 QY 785 ----- 784
 DB 845 GAATTAATAATTAATAAGTACAGTGGGACTGTGCTGCTGCTGCTGCTGCTTTT 904
 QY 785 ----- 784
 DB 905 TCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGATTAAGTCTGATATATGAT 964
 QY 785 ----- 784
 DB 965 ACTAATAGTGAATATATCTTACACATGACTCAGACACACAGTATGTCACAACTTGT 1024
 QY 785 ----- 784
 DB 1025 GCTTTTGACCTAATACCTTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
 QY 785 -----AGCAAGGCGCACAGACATCTAGTGAAGCAA 815
 DB 1085 TGGCAATTTGACCTGGAACACCTTTGCGCAAGCAAGGACAGACATCTAGTGAAGCAA 1144
 QY 816 TTACCGAAGATTGCTCAGAGAGTCTCTCAACATGCTTTGTGCAACAAGATTAAAA 875
 DB 1145 TTACCGAAGATTGCTCAGAGAGTCTCTCAACATGCTTTGTGCAACAAGATTAAAA 1204
 QY 876 GATCTGTGTGTTTTCATGATGATTAATGATGATGATGATGATGATGATGATGAT 935
 DB 1205 GATCTGTGTGTTTTCATGATGATTAATGATGATGATGATGATGATGATGATGAT 1264
 QY 936 AAGAAAGTCTGCTGATGATTTGAAATTTGAATCTCTAGAGTCTGATTAAGTCTG 995
 DB 1265 AAGAAAGTCTGCTGATGATTTGAAATTTGAATCTCTAGAGTCTGATTAAGTCTG 1324
 QY 996 AGGAAATTTGAAGAGCTCAGAGCAAGTTAAATCCCTTTCTTCAAGAAATCTGATGA 1055
 DB 1325 AGGAAATTTGAAGAGCTCAGAGCAAGTTAAATCCCTTTCTTCAAGAAATCTGATGA 1384
 QY 1056 TTTATATGTCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1115
 DB 1385 TTTATATGTCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1444
 QY 1116 TCATATGAAAGAGCAATGAAATTTGATGATGATGATGATGATGATGATGATGAT 1175
 DB 1445 TCATATGAAAGAGCAATGAAATTTGATGATGATGATGATGATGATGATGATGAT 1504
 QY 1176 ACAATCTTGTCTTCTTCTGAGGATCTTACCAAAATGAGCTGGAATGAGCATC 1235
 DB 1505 ACAATCTTGTCTTCTTCTGAGGATCTTACCAAAATGAGCTGGAATGAGCATC 1564
 QY 1236 AATGATGCTGAGACACCAAAAGTAAA 1266
 DB 1565 AATGATGCTGAGACACCAAAAGTAAA 1595
 RESULT 8
 AB224707
 ID AB224707 standard; cDNA; 1773 BP.
 XX
 AC AB224707;
 XX
 DT 07-Apr-2003 (first entry)
 XX
 DE Human cell growth, differentiation and death protein CGPD-19 cDNA.
 XX
 XX CGPD-19; cell growth; cell differentiation; cell death; human;
 KW cytosolic; antiarteriosclerotic; hepatotropic; antiinflammatory;
 KW antiproliferative; antianemic; ophthalmological; auditory; anticonvulsant;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW neuroleptic; tranquilizer; immunosuppressive; anti-HIV; antiallergic;
 KW antiaesthetic; antihypertensive; antidiabetic; dermatological; nephrotoxic;
 KW antineumatic; antiarthritic; antitumor; antineoplastic; antineoplastic;
 KW antibacterial; fungicide; antiparasitic; protozoicide; antihelminthic;

Db 1160 AAAAGAAAGCTGGCTGATGATTTGAAATTGATCTCTAGAGTGGTGATGAAGTCT 1219
QY 995 GAGGAAATTTGAGAGCTGACGAGCAACGTTAAATCCCTTTCTTACGAAATTCCTGATGA 1054
Db 1220 GAGGAAATTTGAGAGCTGACGAGCAACGTTAAATCCCTTTCTTACGAAATTCCTGATGA 1279
QY 1055 ATTATATGTCCTCAATGAGAGCTTATGAAAGATCCCGTCTATCCATCAGATGGCTA 1114
Db 1280 ATTATATGTCCTCAATGAGAGCTTATGAAAGATCCCGTCTATCCATCAGATGGCTA 1339
QY 1115 TTGATATGAAAGAGCAATGGAATAATGGATCAGCAAAAAGAAAGCTACAGTCCCAT 1174
Db 1340 TTGATATGAAAGAGCAATGGAATAATGGATCAGCAAAAAGAAAGCTACAGTCCCAT 1399
QY 1175 GACAAATCTTGTCTTCTTCTTCCAGGCTACTTACCAAAATGAGCTCTGAAATGGCCAT 1234
Db 1400 GACAAATCTTGTCTTCTTCTTCCAGGCTACTTACCAAAATGAGCTCTGAAATGGCCAT 1459
QY 1235 CAATGATGGCTGGAGACACACCAAAAGTAA 1266
Db 1460 CAATGATGGCTGGAGACACCAAAAGTAA 1491

RESULT 9
ADB63535
ID ADB63535 standard; cDNA; 1811 BP.
XX ADB63535;
AC
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone TBEST120264530.
XX
KW Human; ss: gene; pharmaceutical; diagnostic; gene therapy;
KW tissue regeneration; cell regeneration; membrane protein;
KW signal transduction-related protein; transcription-related protein;
KW osteoporosis; neurological disease; cancer; tumour.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 150..1580
FT CDS /*tag= a
FT /product= "Clone TBEST120264530 protein"
XX
XX EP1308459-A2.
XX
XX PD 07-MAY-2003.
XX
XX PF 28-MAR-2002; 2002EP-00007401.
XX
XX PR 05-NOV-2001; 2001JP-00379298.
XX PR 25-JAN-2002; 2002US-00350978.
XX
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX PI Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WP1: 2003-450961/43.
XX
XX P-PSDB: ADB65505.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
XX marker or medicines for regulation of their expression and activity, or
XX as targets of gene therapy.
XX
XX Claim 1; Page: 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
XX from 1970 fully defined nucleotide sequences which encode novel

CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or peptide
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesizing the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.
XX
SQ Sequence 1811 BP; 520 A; 352 C; 399 G; 540 T; 0 U; 0 Other;

Query Match 70.0%; Score 890.2; DB 10; Length 1811;
Best Local Similarity 80.9%; Pred. No. 2.4e-261;
Matches 1178; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 86 GGCTGTTTTCTTCAATAAAGAACATGTGAACCTGATTCACACATTAGCTGATCAG 145
Db 125 GGCTGTTTTCTTCAATAAAGAACATGTGAACCTGATTCACACATTAGCTGATCAG 184
QY 146 TGAGAGATGCACTGCTGTCGCTTCTTCCCTTTCCCTCTTGCTGCTGCTGCA 205
Db 185 TGAGAGATGCACTGCTGTCGCTTCTTCCCTTTCCCTCTTGCTGCTGCTGCA 244
QY 206 AACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265
Db 245 AACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
QY 266 TCATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325
Db 305 TCATACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
QY 326 TTCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 385
Db 365 TTCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
QY 386 GGAACAGCTAGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
Db 425 GGAACAGCTAGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484
QY 446 GGCATCAGGGGCAAGCTGATGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505
Db 485 GGCATCAGGGGCAAGCTGATGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 506 TAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 565
Db 545 TAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
QY 566 CTTCTTTGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
Db 605 CTTCTTTGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 664
QY 626 TCTGATAGTGAAGAAAGCAATGATCTTGAATTAATCTGCTGCTGCTGCTGCTGCTG 685
Db 665 TCTGATAGTGAAGAAAGCAATGATCTTGAATTAATCTGCTGCTGCTGCTGCTGCTG 724
QY 686 AGTTCTGATGGAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
Db 725 AGTTCTGATGGAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 784
QY 746 CCAAGTCAAAATTTGATGTTGTTCTTTACCATATCTT----- 784

Db 785 CCAAGTCAAAATTGGATGTTCTTTCTTTTACCAATCTTAGTTTGATTAATAATTA 844
QY 785 ----- 784
Db 845 AAGTACACTGATGGGCACTGTCTCTCTGCTTTGCGCTTGTGCTTTTCCCATGATGGCA 904
QY 785 ----- 784
Db 905 GATGCTAGTCTCAGGGCTCAGTGATAGTCTGTCTATATGATATGATCTAATACTAGAA 964
QY 785 ----- 784
Db 965 TATACCTTACACATTTGACTGAGCACACAGGTATGTCACAACTTGTCTTTTGACCTAA 1024
QY 785 ----- 784
Db 1025 TACCTTTTACTTCTGCTACTGTTTCATATGACAAAACAGTACATCTGCAATTTGACCT 1084
QY 785 -----AGCAAGGGGCAAGAACATCAGCTGAGCAATTTACCGAAGATTG 829
Db 1085 GGAACACTTTGCCAGACAGAGACAGACAGAACATCAGCTGAGCAATTTACCGAAGATTG 1144
QY 830 GTCAGAGAGAGTGTCTCAACATGTGCTTTTGTGCAACAAGATTTTAAAGATCTTGTGTAT 889
Db 1145 GTCAGAGAGAGATGTCTCAACATGTGCTTTTGTGCAACAAGATTTTAAAGATCTTGTGTAT 1204
QY 890 TTTTCAGATGATTAATTAATCTCTAGAGACTGCGTAGTAAGTGTGTGAGAAAATTGAGA 1009
Db 1205 TTTTCAGATGATTAATTAATCTCTAGAGACTGCGTAGTAAGTGTGTGAGAAAATTGAGA 1009
QY 950 TGAATGATTTGAAAAATTGAATCTCTAGAGACTGCGTAGTAAGTGTGTGAGAAAATTGAGA 1009
Db 1265 TGATGATTTGAAAAATTGAATCTCTAGAGACTGCGTAGTAAGTGTGTGAGAAAATTGAGA 1324
QY 1010 GCTCAGAGACCAAGTTAAATCCCTTTCTTCAGGAATTCCTGATGATTTAATATGCCAAT 1069
Db 1325 GCTCAGAGACCAAGTTAAATCCCTTTCTTCAGGAATTCCTGATGATTTAATATGCCAAT 1384
QY 1070 AACTAGAGAACTTATGAAAANTCCGTCATCGCATCGCATGAGTATTCATATGAAAAAGA 1129
Db 1385 AACTAGAGAACTTATGAAAANTCCGTCATCGCATCGCATGAGTATTCATATGAAAAAGA 1444
QY 1130 AGCAATGGAATTTGATCGACAAAAAGAAAGTACAAAGTCCCATGACAAATCTTGTCT 1189
Db 1445 AGCAATGGAATTTGATCGACAAAAAGAAAGTACAAAGTCCCATGACAAATCTTGTCT 1504
QY 1190 TCCCTTACGCGTACTTACACCAATAGAGCTTGAAAAATGCGCATCAATAGATGGCTGA 1249
Db 1505 TCCCTTACGCGTACTTACACCAATAGAGCTTGAAAAATGCGCATCAATAGATGGCTGA 1564
QY 1250 GACACACCAAAAGTAA 1266
Db 1565 GACACACCAAAAGTAA 1581

RESULT 10
ABV29028
ID ABV29028 standard; cDNA; 1996 BP.
XX
AC ABV29028;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 29019.
XX
KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenetic marker; gene; ss.
OS Homo sapiens.
XX
PN MO200160860-A2.
XX

PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1, Page 6145-6146; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification of its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (1) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other;
XX
Query Match 69.1%; Score 878.8; DB 5; Length 1996;
Best Local Similarity 80.7%; Pred. No. 7.9e-258;
Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1;
QY 99 CAAATTAAGAACATGTGTGAATGATTCACATTAAGTATGATCATGTGACATGTCAAC 158
Db 4 CAAATTAAGAACATGTGTGAATGATTCACATTAAGTATGATCATGTGACATGTCAAC 63
QY 159 TCGTGTGCTTCTCTTTTCCCTCTTGTGCTACTTGTCTCTTGACAAAACATTTGCCCTG 218
Db 64 TCGTGTGCTTCTCTTTTCCCTCTTGTGCTACTTGTCTCTTGACAAAACATTTGCCCTG 123
QY 219 TACTGTTACGTGACTTACTGAACTGCAATTCCTCAATTGAAAGTTTCAATCTATGCT 278
Db 124 TACTGTTACGTGACTTACTGAACTGCAATTCCTCAATTGAAAGTTTCAATCTATGCT 183
QY 279 GTCCACTGTGCTGTCTTCTCCCTTCAGAGACATATTTTGGCATTCGTGTTCAACAGATGT 338
Db 184 GTCCACTGTGCTGTCTTCTCCCTTCAGAGACATATTTTGGCATTCGTGTTCAACAGATGT 243
QY 339 ACCACTGTCTTATGAAATCTGAAAAATGACACAGATGCTGACGTGATGAAACAGCTTACT 398
Db 244 ACCACTGTCTTATGAAATCTGAAAAATGACACAGATGCTGACGTGATGAAACAGCTTACT 303
QY 399 GGCAGCCCTGTGAGGGTTTGGCAGTTTCCCAAGTCCACAGTGTGTTGGCATCAGGGGCA 458
Db 304 GGCAGCCCTGTGAGGGTTTGGCAGTTTCCCAAGTCCACAGTGTGTTGGCATCAGGGGCA 363
QY 459 GCTGATGAACTGTGTTTGTGGAATGACAGTCAATACAAATTAATATGATGTGTAGT 518
Db 364 GCTGATGAACTGTGTTTGTGGAATGACAGTCAATACAAATTAATATGATGTGTAGT 423
QY 519 GTTAAAGATGGCTCTTGGCGGAGTGTGATTTTCTCTTAATGAAAGCTTTCTTGTGACT 578
Db 424 GTTAAAGATGGCTCTTGGCGGAGTGTGATTTTCTCTTAATGAAAGCTTTCTTGTGACT 483

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QY 579 GGCCTCATGTGGTGAATTTAAAGTGGGATGATAAATAGAGTGTCTGATAGTGA 638
DB 484 GGGCTTCATGATGGATTTAAGTGGGATGATAAAGAGGTGTCTGATAGTGA 543
QY 639 AAGACATGATCTTGGAAATTAACCTGCTGCAATTTTCTTCAAGCCAGTTTCTGATGA 698
DB 544 AAGACATGATCTTGGAAATTAACCTGCTGCAATTTTCTTCAAGCCAGTTTCTGATGA 603
QY 699 GAACAAGTCTTCAAGTTTTCAGTGCATCATGTGTCAGATTGCGAAGTCAAAAT 758
DB 604 GAACAAGTCTTCAAGTTTTCAGTGCATCATGTGTCAGATTGCGAAGTCAAAAT 663
QY 759 TGGATTGTTCTTTACCAATATCTT----- 784
DB 664 TGGATTGTTCTTTACCAATATCTT----- 723
QY 785 ----- 784
DB 724 GGGCAGTGTGCTCTGTTCTGGCTTGTGCTTTTCCCATGATGGGAGAGTCTAGTCTCA 783
QY 785 ----- 784
DB 784 GGGTCAAGTGAATAGTCTGATAGTATAGTATACTAATAGTGAATATATCTTCAACA 843
QY 785 ----- 784
DB 844 TTGACTACGACACACAGGATATGTCAACAATTGTGCTTTTGCACTTAATACCTTTTACTT 903
QY 785 ----- 784
DB 904 GCTACTGGTTCAATGACAAAGAGTGAACATCTGGCAATTTGACTGGAAACACTTTGC 963
QY 785 --ACGAAGGGCCACAGAAACATCAGCTGAGCAATTTACCGAAGTTGGTCAAGAGGTC 842
DB 964 CAAGCAAGGGCCACAGAAACATCAGCTGAGCAATTTACCGAAGTTGGTCAAGAGGAT 1023
QY 843 GTCTCAACATGGCTTTGTGCAAGATTTAAAGATCTTGTGATTTTCAAGATGAAT 902
DB 1024 GTCTCAACATGGCTTTGTGCAAGATTTAAAGATCTTGTGATTTTCAAGATGAAT 1083
QY 903 AACATGATGAGAAAGAACTGTTGAATCTTACAAAGAAAGTCTGGCTGATGATTTGAA 962
DB 1084 AACATGATGAGAAAGAACTGTTGAATCTTACAAAGAAAGTCTGGCTGATGATTTGAA 1143
QY 963 ATTGAATCTCTAGAGCTGCTGATGAAGTCTGAGAAATTTGAAGAGCTCAGACCAAG 1022
DB 1144 ATTGAATCTCTAGAGCTGCTGATGAAGTCTGAGAAATTTGAAGAGCTCAGACCAAG 1203
QY 1023 GTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTAATGTCGAATTAACAGAACTT 1082
DB 1204 GTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTAATGTCGAATTAACAGAACTT 1263
QY 1083 ATGAAGATCCGTCATCGCATGATGATGCTATTCATATGAAGAAAGCAATGGAAT 1142
DB 1264 ATGAAGATCCGTCATCGCATGATGATGCTATTCATATGAAGAAAGCAATGGAAT 1323
QY 1143 TGGATCAGCAAAAGAAAGTCAAGTCCATGACAAATCTTGTCTTCTTCAAGCGTA 1202
DB 1324 TGGATCAGCAAAAGAAAGTCAAGTCCATGACAAATCTTGTCTTCTTCAAGCGTA 1383
QY 1203 CTTACACCAATAGAGCTCTGAAATGAGCCATCAATAGTGGCTGAGAGACACCAAAAG 1262
DB 1384 CTTACACCAATAGAGCTCTGAAATGAGCCATCAATAGTGGCTGAGAGACACCAAAAG 1443
QY 1263 TAAA 1266
DB 1444 TAAA 1447
```

RESULT 11
ABV23190
ID ABV23190 standard; cDNA; 1996 BP.

```
XX AC ABV23190;
XX XX
XX 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 23181.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX FN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183119P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PT Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PT Claim 1; Page 4166-4167; 11750pp; English.
XX PS
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX SQ
XX Sequence 1996 BP; 615 A; 378 C; 447 G; 543 T; 0 U; 13 Other:
XX
XX Query Match 69.1%; Score 878.8; DB 5; Length 1996;
XX Best Local Similarity 80.7%; Pred. No. 7.9e-258;
XX Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1.
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Db      244  ACCAGTCTCTATGGAATACTGAAAAATGACAGATGCTGCAAGATGAAAGACCTAGT 303
Qy      399  GGGAGCCCTGTGAGGGCTTTGCCAGTTTCCCGACAGCTCCACGTTTGGATCAGGGGCA 458
Db      304  GGGAGCCCTGTGAGGGCTTTGCCAGTTTCCCGACAGCTCCACGTTTGGATCAGGGGCA 363
Qy      459  GCTGATGAACTGTGGTTTGTGGAATGACAGATCATACAATTTATATAGATGTGAGT 518
Db      364  GCTGATGAACTGTGGTTTGTGGAATGACAGATCATACAATTTATATAGATGTGAGT 423
Qy      519  GTTAAAGATGGCTCTTGGCGGCAATGCAATTTCTCTAATGGAAGCTTCTTGTCACT 578
Db      424  GTTAAAGATGGCTCTTGGCGGCAATGCAATTTCTCTAATGGAAGCTTCTTGTCACT 483
Qy      579  GGGTCCCTCATGTGTGATTTAAACAGTGTGGATGATPAAATGAGGTCTGCATAGTGA 638
Db      484  GGGTCCCTCATGTGTGATTTAAACAGTGTGGATGATPAAATGAGGTCTGCATAGTGA 543
Qy      639  AAGACATGATCTTGGAAATTAACCTGCTGCATTTTCTTCAAGCCAGTTTCTGATGA 698
Db      544  AAGACATGATCTTGGAAATTAACCTGCTGCATTTTCTTCAAGCCAGTTTCTGATGA 603
Qy      699  GAAACAAGCTTCAAGTTTTCGACCTGCAATCATGTGTCAGAGATTGCCAAGTCAAAAT 758
Db      604  GAAACAAGCTTCAAGTTTTCGACCTGCAATCATGTGTCAGAGATTGCCAAGTCAAAAT 663
Qy      759  TGGATGTTCTTCTTCCCATCTT----- 784
Db      664  TGGATGTTCTTCTTCCCATCTTAAAGTTTGAATTAATAATATAAGTACATGAGT 723
Qy      785  ----- 784
Db      724  GGGCAGCTGCTCCTGTTGGCTTGTGCTTTTCCCATGATGGCGAGATGCTAGTCTCA 783
Qy      785  ----- 784
Db      784  GGGTCAGTGAATAAGTCTCATAGTATATGATACTAATAGTGAATATACTTACACACA 843
Qy      785  ----- 784
Db      844  TTGACTCAGACACCAAGTATGTCAACAATTTGCTTTGCACTTAATCCCTTTTACTT 903
Qy      785  ----- 784
Db      904  GCTACTGTTCAATGACAAAAACAGTGAACATCTGCAATTTGACCTGGAACAATTTGC 963
Qy      785  --AGCAAGGGCGACACAGAACTCAGCTGAGCAATTTACCGAAGTTGGTCAGAGAGGTC 842
Db      964  CAAGCAAGGGCGACAGAACTCAGCTGAGCAATTTACCGAAGTTGGTCAGAGAGGAT 1023
Qy      843  GTCTCAACATGGCTTTGTGACAAAGATTAAAGATCTTGTGGTATTTTCAAGATGAAT 902
Db      1024  GTCTCAACATGGCTTTGTGACAAAGATTAAAGATCTTGTGGTATTTTCAAGATGAAT 1083
Qy      903  AACATTGATGAAAAAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAA 962
Db      1084  AACATTGATGAAAAAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAA 1143
Qy      963  ATTGAATCTTAAAGACTGCTAGTAAAGTCTGAGGAAAAATTGAAGGCTCAGAGACCAAG 1022
Db      1144  ATTGAATCTTAAAGACTGCTAGTAAAGTCTGAGGAAAAATTGAAGGCTCAGAGACCAAG 1203
Qy      1023  GTTAAATCCCTTTCTTCAAGAAATCCGATGAATTTTATATGTCCAATTAAGTGAAGAACT 1082
Db      1204  GTTAAATCCCTTTCTTCAAGAAATCCGATGAATTTTATATGTCCAATTAAGTGAAGAACT 1263
Qy      1083  ATGAAGATCCGTCATCGCATGATGATGCTATTCATATGAAAAAGAAAGCATGGAAT 1142
Db      1264  ATGAAGATCCGTCATCGCATGATGATGCTATTCATATGAAAAAGAAAGCATGGAAT 1233
Qy      1143  TGGATCAGCAAAAAGAAAGTACAGTCCATGACAAATCTTGTCTTCTTCAAGCGGTA 1202

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Db      1324  TGGATCAGCAAAAAGAAAGCTACAAAGTCCCATGACAAATCTTGTCTTCTTCAAGCGGTA 1383
Qy      1203  CTTACACCAAAATGGAATCTGAAAAATGGCCATCAATAGTGTGAGACACACCAAAAG 1262
Db      1384  CTTACACCAAAATGGAATCTGAAAAATGGCCATCAATAGTGTGAGACACACCAAAAG 1443
Qy      1263  TAAA 1266
Db      1444  TAAA 1447

RESULT 12
AAD45076
ID AAD45076 standard; DNA; 1908 BP.
XX
AC AAD45076;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human RET16.3 splice variant DNA.
XX
KW Human; RET16; intracellular signal; inflammation-related disease; asthma;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; neuroprotective;
KW transplant rejection; chronic obstructive pulmonary disease; TNF-alpha;
KW inflammatory bowel disease; Crohn's disease; immunosuppressive; cancer;
KW inactive respiratory distress syndrome; cardiac; ulcerative colitis;
KW autoimmune disease; cystic fibrosis; gene therapy; cytostatic; neoplasm;
KW cellular migration disorder; cell proliferation disorder; calcification;
KW hyperinulinaemia; diabetes type 2; systemic lupus erythematosus; tumour;
KW cardiovascular disease; Wegener's granulomatosis; atherosclerosis;
KW thalassemia; vasotropic; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 136..1644
FT FT /tag= a
FT FT /product= "Human RET16.3 splice variant protein"
XX
PN WO200266494-A2.
XX
PD 29-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005162.
XX
PR 16-FEB-2001; 2001US-0269366P.
PR 29-MAY-2001; 2001US-0294181P.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA
PI Todderud CG, Finger JN, Rillema J;
PI
PI WPI; 2002-682760/73.
DR P-PSDB; AAE82168.
XX
PT New human, mouse or rat RET16 genes and proteins, involved in
PT intracellular signaling cascade, useful for in gene therapy, particularly
PT for treating e.g. ischemia, cystic fibrosis, autoimmune disease,
PT tumors or neoplasms.
XX
PS Claim 1; Page 168-169; 175pp; English.
XX
CC The invention relates to human, mouse or rat RET16 genes and proteins,
CC involved in intracellular signaling cascade. The RET16 protein or
CC polynucleotide is useful for treating an inflammation-related disease or
CC disorder, e.g. rheumatoid arthritis, juvenile arthritis, psoriasis,
CC asthma, ischaemia-reperfusion, multiple sclerosis, rejection of organ or
CC tissue transplants, chronic obstructive pulmonary disease, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, inactive respiratory
CC distress syndrome, systemic lupus erythematosus, autoimmune disease,
CC cystic fibrosis, cancers, tumours or neoplasms. This inflammation-related
CC disease or disorder also includes disorders associated with aberrant
CC activation of the TNF-alpha pathway, disorders associated with aberrant

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cellular migration, proliferation, metastasis, juvenile idiopathic
 arthritis, haemogenous metastases of tumour cells, hyperinsulinemia,
 diabetes type 2, atherosclerosis, cardiovascular disease, colon cancer,
 tumour progression, Wegener's granulomatosis, stem cell transplantation
 complications, ischaemia-reperfusion injury, thalassemia, acute lung
 injury, graft rejection, ischaemic heart, coronary artery calcification
 or allergic inflammation. RET16 DNA is used in gene therapy. The present
 sequence is human RET16.3 splice variant DNA

XX Sequence 1908 BP; 550 A; 399 C; 405 G; 554 T; 0 U; 0 Other;

Query Match 69.0%; Score 877.8; DB 6; Length 1908;

Best Local Similarity 77.9%; Pred. No. 1.6e-257;

Matches 1253; Conservative 0; Mismatches 2; Indels 354; Gaps 2;

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QY 12 TCACCTGCGGGGCGACGTGACCCGCGCGGCGGCACTTGAAGCGGATCCCGGCG 71
DB 37 TCACCTGCGGGGCGACGTGACCCGCGCGGCGGCACTTGAAGCGGATCCCGGCG 96
QY 72 CCCCCGCTCGCGAGCGCTTTTCTCAATAAAGAAAGATGGAACATGATTCACACA 131
DB 97 CCCCCGCTCGCGAGCGCTTTTCTCAATAAAGAAAGATGGAACATGATTCACACA 156
QY 132 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
DB 157 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 216
QY 192 TGCTCTTGGAACAACAATTCGCTGATCTGATGATGATGATGATGATGATGATGAT 251
DB 217 TGCTCTTGGAACAACAATTCGCTGATCTGATGATGATGATGATGATGATGATGAT 276
QY 252 TCTCCATTGAAGTTTCTTACTATGCTGATGATGATGATGATGATGATGATGATGAT 311
DB 277 TCTCCATTGAAGTTTCTTACTATGCTGATGATGATGATGATGATGATGATGATGAT 336
QY 312 ATTTGGCATGCTGTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
DB 337 ATTTGGCATGCTGTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 396
QY 372 ATGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
DB 397 ATGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456
QY 432 GACTCCACGTTGTTGGATCAGGGGCGAGCTGATGATGATGATGATGATGATGATGAT 491
DB 457 GACTCCACGTTGTTGGATCAGGGGCGAGCTGATGATGATGATGATGATGATGATGAT 516
QY 492 TCATACAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 517 TCATACAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
QY 552 TCTCTTAATGAGAGCTTTCTTCTGCTGCTCTCATGATGATGATGATGATGATGATGAT 611
DB 577 TCTCTTAATGAGAGCTTTCTTCTGCTGCTCTCATGATGATGATGATGATGATGATGAT 636
QY 612 GATTAATGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
DB 637 GATTAATGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
QY 672 TTTTCTTCAAGCAGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 731
DB 697 TTTTCTTCAAGCAGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
QY 732 TGTGTCAGAGTTGCCAAGTCAAAATTTGATGATGATGATGATGATGATGATGATGAT 784
DB 757 TGTGTCAGAGTTGCCAAGTCAAAATTTGATGATGATGATGATGATGATGATGATGAT 816
QY 785 ----- 784
DB 817 GAATTAATAATTAAGTACAGTGAAGGCACTGTGCTCTGTGCTGTGCTGTGCTTTT 876
QY 785 ----- 784

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DB 877 TCCCATGATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 936
QY 785 ----- 784
DB 937 ACTAATGATGAGATATATCTTCAACATTTGATGATGATGATGATGATGATGATGAT 996
QY 785 ----- 784
DB 997 GCTTTTGACCTAATACCTTTTACTTCTGATGATGATGATGATGATGATGATGATGAT 1056
QY 785 -----AGAAGGCGCAGAAATCATGATGATGATGATGATGATGATGATGATGAT 815
DB 1057 TGGCAATTTGACCTGGAACACTTTTGGCAGCAAGGCGCAGAAATCATGATGATGATGAT 1116
QY 816 TTTTACCGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
DB 1117 TTTTACCGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176
QY 876 GATCTGTTGATATTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 935
DB 1177 GATCTGTTGATATTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1236
QY 936 AAGAAAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
DB 1237 AAGAAAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1296
QY 967 -----AATCTTGA 977
DB 1297 ACTGCACTTCAACCTCTGCTGCTCAAGTATCTCTTACTGCTGCTGCTGCTGCTGCTG 1356
QY 978 CTGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1037
DB 1357 CTGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1416
QY 1038 TCAAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1097
DB 1417 TCAAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1476
QY 1098 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1157
DB 1477 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1536
QY 1158 AAGCTCAAGTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
DB 1537 AAGCTCAAGTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1596
QY 1218 ACTCTGAAAAATGCGCATCAATAGATGATGATGATGATGATGATGATGATGATGAT 1266
DB 1597 ACTCTGAAAAATGCGCATCAATAGATGATGATGATGATGATGATGATGATGATGAT 1645

```

RESULT 13

AA160662/C
 ID AA160662 standard; cDNA; 1826 BP.

AA160662;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4651.

Human; noctropie; immunosuppressant; cytostatic; gene therapy; cancer;
 peripheral nervous system neuropathy; central nervous system; CNS;
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
 chemokine; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia; ss.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

XX 26-DEC-2000; 2000MO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QJ,
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX MPI; 2001-442253/47.
XX P-PSDB; AAM41506.
XX
PT Novel nucleic acid and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Claim 1; SEQ ID NO 4651; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemoclastic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 1826 BP; 535 A; 382 C; 380 G; 529 T; 0 U; 0 Other;
XX
XX
XX Query Match 68.2%; Score 867.8; DB 4; Length 1826;
XX Best Local Similarity 79.6%; Pred. No. 1.8e-254;
XX Matches 1232; Conservative 0; Mismatches 27; Indels 288; Gaps 6;
XX
QY 12 TCACCTGCGCGGACGTGACCCGACCGCCGCGGACCTTGAAGCGGATCCCGGCG 71
DB 1800 TCACCTGCGCGGACGTGACCCGACCGCCGCGGACCTTGAAGCGGATCCCGGCG 1741
QY 72 CCCCCGCTCTGCAAGCGCTGTTTTCTTCAATAAAGAAATGTTGAATGATTACACA 131
DB 1740 CCCCCCTCTGCAAGCGCTGTTTTCTTCAATAAAGAAATGTTGAATGATTACACA 1681
QY 132 TTAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 131
DB 1680 TTAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1621
QY 192 TGTCTCTTGACAAACAAATTCGCTGTACTGTTACGTTACGTTACGTTACGTTACGTTAC 251
DB 1620 TGTCTCTTGACAAACAAATTCGCTGTACTGTTACGTTACGTTACGTTACGTTACGTTAC 1561
QY 252 TGTCTCTTGACAAATTCGTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 311
DB 1560 TGTCTCTTGACAAATTCGTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1501
QY 312 ATTTTGGCATGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
DB 1500 ATTTTGGCATGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441

QY 372 ATGCTGCAGATGATGAGACAGCCTAGTGGCAGCCGTGAGGGTTTGCCAGTTTCCCA 431
DB 1440 ATGCTGCAGATGATGAGACAGCCTAGTGGCAGCCGTGAGGGTTTGCCAGTTTCCCA 1381
QY 432 GACTCCAGCTGTTTGGCATCAGGGGAGCTGATGAACTGTGTTTGTGAAATGACAG 491
DB 1380 GACTCCAGCTGTTTGGCATCAGGGGAGCTGATGAACTGTGTTTGTGAAATGACAG 1321
QY 492 TCATCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 1320 TCATCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1261
QY 552 TCTCTTAATGAAAGCTTCTTGTGCTGCTCTCTCAATGATGATTAACAGTGGGAT 611
DB 1260 TCTCTTAATGAAAGCTTCTTGTGCTGCTCTCTCAATGATGATTAACAGTGGGAT 1201
QY 612 GATTAATGAGTGTCTGATGATGAAAGACATGATCTTGGAAATTAACCTGCTCGAT 671
DB 1200 GATTAATGAGTGTCTGATGATGAAAGACATGATCTTGGAAATTAACCTGCTCGAT 1141
QY 672 TTTTCTTCAAGCAGCTTTCTGATGAGAACAAAGTCTTCAATTTTGGATGATGATGATGATGAT 731
DB 1140 TTTTCTTCAAGCAGCTTTCTGATGAGAACAAAGTCTTCAATTTTGGATGATGATGATGATGAT 1081
QY 732 TGTGTCAGGATGGCCAAATCAAAATTTGATGTTCTTTTACCATACTT----- 784
DB 1080 TGTGTCAGGATGGCCAAATCAAAATTTGATGTTCTTTTACCATACTT----- 1021
QY 785 ----- 784
DB 1020 GAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 961
QY 785 ----- 784
DB 960 TCCCATGATGGCAGATGCTAGTCTGAGGCTCAGTGGATTAAGTCTGTCAATGATTAATGAT 901
QY 785 ----- 784
DB 900 ACTAATAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 841
QY 785 ----- 784
DB 840 GCTTTTGAACCTAATACCTTTTACTTGTCTAGTCTGATGATGACAAACAGTGAACATC 781
QY 785 -----AGCAGGCGCACGAACATCAGCTGAAGCAA 815
DB 780 TGCGAATTTGACCTGGAACACTTTTGCCAAAGCAGGACGAAACATCAGCTGAAGCAA 721
QY 816 TTACCGAAGATTGTCAGAGAGATGCTCTCAACATGCTTGTGTCACAAAGATTTTAA 875
DB 720 TTACCGAAGATTGTCAGAGAGATGCTCTCAACATGCTTGTGTCACAAAGATTTTAA 661
QY 876 GATCTTGTGTTATTTTCAAGATGAATTAACATTTGATGAAAGAACTGTTGAATCTTTACA 935
DB 660 GATCTTGTGTTATTTTCAAGATGAATTAACATTTGATGAAAGAACTGTTGAATCTTTACA 601
QY 936 AAGAAAGTCTGCTGATGATTTGAAATGAAATCTCTGAGATGCTGCTGTAAGTGAAGTCTG 995
DB 600 AAGAAAGTCTGCTGATGATTTGAAATGAAATCTCTGAGATGCTGCTGTAAGTGAAGTCTG 541
QY 996 AAGAAATTTGAAGCTCAGAACCAAGTTAAATCCCTTTTTCAGAAATTCCTGATGA 1055
DB 540 AAGAAATTTGAAGCTCAGAACCAAGTTAAATCCCTTTTTCAGAAATTCCTGATGA 481
QY 1056 TTTATATGTCATTAATCTAGAGAACTTAATGAAGATCCGCTCATGCCATCAAGTGGCTAT 1115
DB 480 TTTATATGTCATTAATCTAGAGAACTTAATGAAGATCCGCTCATGCCATCAAGTGGCTAT 421
QY 1116 TCATATGAAGAAAGACATGAAATTTGG--ATCAGCAAAAAAGAA--GATACAGTCCC 1172
DB 420 TCATATGAAGAAAGACATGAAATTTGGATTCAGCAAAAAAGAA--GATACAGTCCC 361
QY 1173 ATGACAAATCTTGTCTTCTT-----CAGCGGTAC--TTACACCAATAAGACATCTGA 1224

Db 1381 GTFAA 1385
|||||
RESULT 15
ADM19385
ID ADM19385 standard; cDNA; 1686 BP.
XX
AC ADM19385;
XX
DT 20-MAY-2004 (first entry)
XX
DE Novel human channel/transporter gene #182.
XX
KW da; Gene; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cycostatic; cardiant; vasotrophic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KW optalmological; gene therapy; channel/transporter protein;
KW rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder;
KW cerebral ischemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.
XX
OS Homo sapiens.
XX
PN WO200154472-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001307.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218280P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476159/51.
XX DR P-PSDB; ADML9864.
XX
PT Isolated nucleic acid molecule encoding a channel/transporter protein is
XX used in preventing, treating or ameliorating a medical condition.
XX
PS Claim 1; SEQ ID NO 192; 809pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding a
CC channel/transporter protein or sequences at least 95% identical to a
CC these. The nucleic acids and proteins encoded by them are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. The antibodies to the proteins can also be used
CC in alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunoassays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
CC The polypeptides can also be used to aid wound healing and epithelial
CC cell proliferation, to prevent skin aging due to sunburn, to maintain
CC organs before transplantation, for supporting cell culture of primary
CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
CC also be used as a food additive or preservative to increase or decrease
CC storage capabilities. This sequence corresponds to a gene of the
CC invention.
XX
SQ Sequence 1686 BP; 485 A; 348 C; 353 G; 500 T; 0 U; 0 Other;
Query Match 61.5%; Score 782; DB 5; Length 1686;
Best Local Similarity 77.3%; Pred. No. 3.3e-228;
Matches 1075; Conservative 0; Mismatches 180; Indels 135; Gaps 5;
QY 12 TCACCTGGCGGCACTGACCCGCGACCCCGTGGGCACTTGAAGGCGATCCGCGCG 71
DB 51 TCACCTGGCGGCGGACGTGACCCGCGACCCCGTGGGCACTTGAAGGCGATCCGCGCG 110
QY 72 CCCCCGCTCCGCGAGGCTTTTCTTCAATAAAGAACTGGTAACTGATTCACACA 131
DB 111 CCCCCGCTCCGCGAGGCTTTTCTTCAATAAAGAACTGGTAACTGATTCACACA 170
QY 132 TTAGCTGATCATGTGACGATGTCAACTGCTGTGCTTCTCTTCTTCTGCTACT 191
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DB 121 TTAGCTGATCATGTGACGATGTCAACTGCTGTGCTTCTCTTCTTCTGCTACT 230
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:05:29 ; Search time 3079 Seconds
(without alignments)
15725.154 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: gb_est6:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	782	61.5	1600	3	CR619104 full-length
3	767.4	60.3	941	1	AL533510 full-length
4	756.6	59.5	889	1	AL533533 full-length
5	716.6	56.3	1010	4	BM543484 full-length
6	664.2	52.2	858	4	BM543484 full-length
7	627.4	49.3	792	4	BI821143 full-length
8	527.8	41.5	728	7	CN793033 full-length
9	493	38.8	505	1	AI189142 full-length
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15	417.4	32.8	910	5	BQ895162 full-length
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17	393.6	30.9	838	7	CK792250 full-length
18	388.4	30.5	839	7	CK306752 full-length
19	386	30.3	727	7	CK364577 full-length
20	382	30.0	640	6	CB240898 full-length
21	381	30.0	1018	1	AL576357 full-length
22	378.4	29.7	559	4	BI681850 full-length
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33	337.2	26.5	869	5	BU148588
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40	313	24.6	435	2	BE501389
41	310.4	24.4	549	2	BF063606
42	308	24.2	542	2	BE675766
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44	301.6	23.7	590	4	BM076153
45	301	23.7	807	1	AL040518

ALIGNMENTS

RESULT 1	CR607851	1770 bp	RNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CSODN004YJ15 of Adult brain of Homo sapiens (human).				
DEFINITION	CR607851.1 GI:50486659				
ACCESSION	CR607851				
VERSION	HTC; CNSL_CDNA.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1770)				
AUTHORS	Ll,w.B., Gruber,C., Jesssee,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Feng Liang Email: fliang@life.rockefeller.edu http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1770)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqret@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a Noci-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
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	/db_xref="taxon:9606"				
	/clone="CSODN004YJ15"				
	/tissue_type="Adult brain"				
	/plasmid="pCMVSPORT_6"				
Query Match	75.8% Score 964.2; DB 3; Length 1770;				
Best Local Similarity	81.8% Pred. No. 8.5e-265;				
Matches 1252; Conservative	0; Mismatches 3; Indels 276; Gaps 1;				
Db	12 TCACCTGCGCGGCGACGTCGACCGCGCGCGGCGACCTTGAAGCGGATCCGCGCG 71				
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QY	72	CCCCGCGCCGAGGGCGTTTCTTCTTAATTAAGAAACATGGGAAACGTATTCACGA	131
Db	129	CCCCGCTCTTCAGAGCGCTGTTTTTCTTAATAAAGAAACATGGGAAACGTATTCACGA	188
QY	132	TTAGTCGATCATGTGACGATGTCAACTGCTGTGCTTCTCTCTTTCCTCTTGGACTACT	191
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QY	252	TCTCCATTGAAGTTTCATACCTATGCTGTCTCACTGCTCTGTTCTTCCCTTCAGAGACAT	311
Db	309	TCTCCATTGAAGTTTCATACCTATGCTGTCTCACTGCTCTGTTCTTCCCTTCAGAGACAT	368
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Db	369	ATTTTGGCATGCTGTTCACACAGATGTGACCACTGCTCTATGGAATATCTGAAATGTGACAG	428
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Db	429	ATGCGCGAGATGATGGAAACAGCTTATGAGGGACCCCTGTGAGAGGTTTGCACTTTTCCCA	488
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QY	612	GATTAATATGAGGTGTCTGCATATGTGAAGAAAGACATGATCTTGGAATTAACCTGCTGGCAT	671
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Db	789	TGTGTCAAGATTTGCCAAGTCAAAATTTGGATTGTTCTTTTAAACCATATCTTAAAGTTTY	848
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Db	849	GAATTTAAATATATAAAGATACACTGAGTGGGACCTGTGCTCCTGTTCTGGCTTGTGCTT	908
QY	785	-----	784
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Db	969	ACTAATACTGAGAATATATCTTCACACATTGACTCAGACACACAGGATATGTACAACTTGT	1028
QY	785	-----	784
Db	1029	GCTTTTGCACTAATACCTTTTACTTGTCTACTGTGTTCAATGACAAAACAGTGAACTC	1088
QY	785	-----AGCAAGGCGCAGACGAACATCAGCTGAAGCA	815
Db	1089	TGGCAATTTGACCTGGAACAACCTTGGCAAGGAAGGCGCACAGAACATCACTGAAGCA	1148
QY	816	TTTAAACCGAAGATTTGGTCAGAGAGAGTCTCTTCACATAGGCTTTGTGCAACAAATTTTAA	875
Db	1149	TTTAAACCGAAGATTTGGTCAGAGAGAGTCTCTTCACATAGGCTTTGTGCAACAAATTTTAA	1208

Qy	876	GATCTTGGTATTTTTTCAAGATGATAATCATGTAAGAAAGACGTGTGAATCTTACA	935
Db	1209	GATCTTGGTATTTTTTCAAGATGATAATCATGTAAGAAAGACGTGTGAATCTTACA	1268
Qy	936	AAAGAAAGCTGGCGTATGATTTGAAAAATTGATCTCTAGACCTCGTAGTAAAGTGGCTG	995
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Qy	996	AGGAAATTTGAAAGCTCAGAGCAAGTTAAATCCCTTTCTTCAGGAATTCCTGATGAA	1055
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Qy	1056	TTTATATGTCCAATTAATCTAGAGAACTTATGAAGAATCCGCTCATGCAATGGCTAT	1115
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Qy	1116	TCATATGAAAAGGAGCAATGGAATTTGATTCACAAAAAAGAACGTACAGTCCCATG	1175
Db	1449	TCATATGAAAAGGAGCAATGGAATTTGATTCACAAAAAAGAACGTACAGTCCCATG	1508
Qy	1176	ACAAATCTTGTTCTTCTTCCTTCAGCGGTACTTACACCAAAATAGGACTCTGAAAATGGCCATC	1235
Db	1509	ACAAATCTTGTTCTTCTTCCTTCAGCGGTACTTACACCAAAATAGGACTCTGAAAATGGCCATC	1568
Qy	1236	AATGATGCTGTGAGACACACCAAAAGTAA	1266
Db	1569	AATGATGCTGTGAGACACACCAAAAGTAA	1599

RESULT 2	
LOCUS	CR619104
DEFINITION	full-length cDNA clone CSOD1075YB08 of Placenta Cot 25-normalized of Homo sapiens (human) .
ACCESSION	CR619104
VERSION	CR619104.1 GI:50499911
KEYWORDS	HTC; CNSLT_CDN.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li, W.B., Gruber, C., Tesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/InvitrogenCorporation 1600 Faraday Avenue
REFERENCE	2 (bases 1 to 1600)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of invitrogen.
FEATURES	Location/Qualifiers
source	1..1600
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="CSOD1075YB08"
	/tissue_type="Placenta Cot 25-normalized"
	/plasmid="pCMVSPORT_6"
ORIGIN	
Query Match	61.5% ; Score 782 ; DB 3 ; Length 1600 ;
Best Local Similarity	77.3% ; Pred. No. 1,6e-212 ;
Matches 1075 ; Conservative	0 ; Mismatches 180 ; Indels 135 ; Gaps 5 ;

QY 12 TCACCTGCGGGGACGTCGACCCGACCGCCGTCGGGACCTTGAAGGCGGATCCCGGCG 71
 DB 13 TCACCTGCGGGGACGTCGACCCGACCGCCGTCGGGACCTTGAAGGCGGATCCCGGCG 72.
 QY 72 CCCCCTCTCTGAGGCTGTTTTTTCTTCAATAAAGAACTGGTGAATGATTCACACA 131
 DB 73 CCCCCTCTCTGAGGCTGTTTTTTCTTCAATAAAGAACTGGTGAATGATTCACACA 132
 QY 132 TTAGCTGATCATGTCGACGATGTCACACTGCTGTCCTTCTCTCTTCCCTTGGGCTACT 191
 DB 133 TTAGCTGATCATGTCGACGATGTCACACTGCTGTCCTTCTCTCTTCCCTTGGGCTACT 192
 QY 192 TGTCTCTTGGACAAACAATTCGCTGTACTGCTTACGTAAGTACTGAAGTGGACAT 251
 DB 193 TGTCTCTTGGACAAACAATTCGCTGTACTGCTTACGTAAGTACTGAAGTGGACAT 252
 QY 252 TCTCCATTGAAGTTTCATATACCTATGCTGTCACCTGCTGCTGTTCTCCCTTCAGACAT 311
 DB 253 TCTCCATTGAAGTTTCATATACCTATGCTGTCACCTGCTGCTGTTCTCCCTTCAGACAT 312
 QY 312 ATTTTGGCATCTGTTCAACAGATGTCACACTGCTGCTGTTCTCCCTTCAGACAT 371
 DB 313 ATTTTGGCATCTGTTCAACAGATGTCACACTGCTGCTGTTCTCCCTTCAGACAT 372
 QY 372 ATGCTGGCATGATGGAACAGCCCTAGTGGAGCCCTGGAAGGTTTGCAGTTTCCCA 431
 DB 373 ATGCTGGCATGATGGAACAGCCCTAGTGGAGCCCTGGAAGGTTTGCAGTTTCCCA 432
 QY 432 GACTCCACGTTTGGCATGAGGGGACGCTGATGGAACGTTGTTTGTGGAATGACAG 491
 DB 433 GACTCCACGTTTGGCATGAGGGGACGCTGATGGAACGTTGTTTGTGGAATGACAG 492
 QY 492 TCTATCAAAATTATATAGATGTGTGATGTTAAAGATGGCTCTTGGGCGCATGTCAT 551
 DB 493 TCTATCAAAATTATATAGATGTGTGATGTTAAAGATGGCTCTTGGGCGCATGTCAT 552
 QY 552 TCTCCATAATGGAAGCTCTTGTCACTGAGGCTCCCTCATGTTGTTTGAAGTGGAGAT 611
 DB 553 TCTCCATAATGGAAGCTCTTGTCACTGAGGCTCCCTCATGTTGTTTGAAGTGGAGAT 612
 QY 612 GATATAATGAGGTCTGTCATAGTGAAGAAAGCAGATGATCTTGGAAATTAACCTGTCGAT 671
 DB 613 GATATAATGAGGTCTGTCATAGTGAAGAAAGCAGATGATCTTGGAAATTAACCTGTCGAT 672
 QY 672 TTTTCTTCAACAGCAGTTTCTGATGAGAAACAGGCTTCTCAATTTTTCGACTGGCATCA 731
 DB 673 TTTTCTTCAACAGCAGTTTCTGATGAGAAACAGGCTTCTCAATTTTTCGACTGGCATCA 732
 QY 732 TGTGTCAGGATGTCGCAAGTCAAAATTTGATGTTCTTTTACCCATCTTGAAGCAAG 791
 DB 733 TGTGTCAGGATGTCGCAAGTCAAAATTTGATGTTCTTTTACCCATCTTGAAGCAAG 792
 QY 792 CGCAGCAAGATCATGCTGAAGC-----AATTT 818
 DB 793 GAATTAATAATATAAGTACATGAGTGGGACATGTCCTCTGTTCTGGCTGTGCTTTT 852
 QY 819 ACCGAAGATTGGTCAGAGGAGCTC----- 842
 DB 853 TCCCATGATGGGAGATGCTAGTCTCAGGGTCACTGATAGTCTGTCATAGTATATGAT 912
 QY 843 -----GTTCTCAACATG 854
 DB 913 ACTAATATCTAGATATATCTTACACACTTGCACACACAGTATGTCACAACTTGT 972
 QY 855 CTTTTGTGACAGAG-----TTTAAAGATCTTGTGATATTTTCAAGATGAATTAACAT 908
 DB 973 GCTTTTGCACCTAATACCTTTTACTTGTCTGATGCTGTTCAATGACAAACAGTGAACATC 1032
 QY 909 GATGGAAGAAAGCTGTTGATCTTCAAAAGAAAGTCTGGCTGATGATTTGAAATTTGAA 968
 DB 1033 TGGCAATTTTGAACCTGGAAGAACTTTTGGCCAGCAAGGCGCAGAGAACTCAAGCTGAACAA 1092
 QY 969 TCT--CTAGAGCTGCTGATGTTAAAGTGTGAGGAAGAAATTTGAAGAGCTCAGAGCAAGGTTA 1026

DB 1093 TTTACGGAATATGTCGACAGAGATGTCACAACTGCTTTGTGACAAAGATTTTAAA 1152
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 DB 1153 GATCTTGTGTGTTTTCATAGATGAATTAACATGATGGAAGAAAGAACTGTGAATCTTACA 1212
 QY 1087 AA-----GATCCGGTCATGTCATGATGAGGCTATTCATATGAAAGAAAGCAATG 1136
 DB 1213 AAAGAAAGTCTGCTGATGATTTTGAAGATTTGATGCTATTCATATGAAAGAAAGCAATG 1272
 QY 1137 GAAATTTGATTCAGCAAAAGAAAGAAAGCTACAAAGTCCCATGCAAAATCTTGTCTTCTTCA 1196
 DB 1273 GAAATTTGATTCAGCAAAAGAAAGAAAGCTACAAAGTCCCATGCAAAATCTTGTCTTCTTCA 1332
 QY 1197 GCGGTAATTCACCAAAATAGAGCTTGAAGAAAGCCATCAATATGATGCTGAGACACAC 1256
 DB 1333 GCGGTAATTCACCAAAATAGAGCTTGAAGAAAGCCATCAATATGATGCTGAGACACAC 1392
 QY 1257 CAAAAGTAAA 1266
 DB 1393 CAAAAGTAAA 1402

RESULT 3
 LOCUS AL533510 941 bp mRNA linear EST 24-MAR-2004
 DEFINITION AL533510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 CS0DN004YJ15 5-PRIME, mRNA sequence.
 ACCESSION AL533510
 VERSION AL533510.3 GI:45708442
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 941)
 AUTHORS I.J.W.B., Gruber,C., Jessee,J. and Polayres,D.
 TITLE Pull-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:31260591.
 CONTACT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 1653.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0DN004CE080P1&c=1653.r.
 LOCATION/Qualifiers

FEATURES
 source 1..941

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN004YJ15"
 /issue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 60.3%; Score 767.4; DB 1; Length 941;
 Best Local Similarity 98.7%; Pred. No. 2e-208;
 Matches 765; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY	12	TCACCTGGGGGACACGTACCCCGACCGCCGCTGGGACCTTGAAGGGGATCCCGGCG	71
Db	68	TCCTCTGGCGGACGTACGACCCGACCGCCGCTGGGACCTTGAAGGGGATCCCGGCG	127
QY	72	CCCCCGCTCTGCAAGCGCTTTTCTTCAAAATAAGAACATGCTGAAACTGATTCACACA	131
Db	128	CCCCCGCTCTGCMCGCGTGTTTTCTTCAAAATAAGAACATGCTGACACTGATTCACACA	187
QY	132	TTAGTGATCAATGGGACGATGTCAATGCTGTGCTCTCTCTTTTCCCTCTTGCTACT	191
Db	188	TTAGTGATCAATGGGACGATGTCAATGCTGTGCTCTCTCTTTTCCCTCTTGCTACT	247
QY	192	TGCTCTTTGACAAAACAATTCGCTGTACTCTGTACGCTGACTTTACTGAACTGCGACAT	251
Db	248	TGCTCTTTGACAAAACAATTCGCTGTACTCTGTGTACGCTGACTTTACTGAACTGCGACAT	307
QY	252	TCTCTCATTTGAAGTTTCATACCTATGCTGTCCACTGCTGCTGTTTCTCCCTTCAGACAT	311
Db	308	TCTCTCATTTGAAGTTTCATACCTATGCTGTCCACTGCTGCTGTTTCTCCCTTCAGACAT	367
QY	312	ATTTTGGCATGCTGTTTCAACAGATGGTATGCCACTGCTCTATGGAATATCTGAAATGACAG	371
Db	368	ATTTTGGCATGCTGTTTCAACAGATGGTATGCCACTGCTCTATGGAATATCTGAAATGACAG	427
QY	372	ATGCTGCGATGATGGAACACGCTTAGTGGCAGCCCTGTGAAGGTTTGGCAGTTTCCCA	431
Db	428	ATGCTGCGATGATGGAACACGCTTAGTGGCAGCCCTGTGAAGGTTTGGCAGTTTCCCA	487
QY	432	GACTCCACGCTTTTGGCATCAAGGGGACACTATGGAACATGAGTGTTTTGGAAATGACAG	491
Db	488	GACTCCACGCTTTTGGCATCAAGGGGACACTATGGAACATGAGTGTTTTGGAAATGACAG	547
QY	492	TCATACAAATATATATAGATGTGTATGTTTAAAGATGGCTCCTTGGCGGACATGTGCATT	551
Db	548	GCATACAAATATATATAGATGTGTATGTTTAAAGATGGCTCCTTGGCGGCMGTGTCAATT	607
QY	552	TCTCTCTAATGGAAGCTTTCTTGTCTACCTGGCTCTCATGTGCTGATTTAAACATGTGGAT	611
Db	608	TCTCTCTAATGGAAGCTTTCTTGTCTACCTGGCTCTCATGTGCTGATTTAAACATGTGGAT	667
QY	612	GATAAATAAGAGGTGTCTGCATAGTAAATAAGACACATGATCTTGAATTAACGTGCGCAT	671
Db	668	GATAAATAAGAGGTGTCTGCATAGTAAATAAGACACATGATCTTGAATTAACGTGCGCAT	727
QY	672	TTTTCTTACACGCCAGTTTCTGTATGAGAAACAAGTCTTCAAGTTTTCGACTGGCATCA	731
Db	728	TTTTCTTACACGCCAGTTTCTGTATGAGAAACAAGTCTTCAAGTTTTCGACTGGCATCA	787
QY	732	TGTGTGTCAGATTTGGCAAGTCAAAATTTGGATGTGTTCTTTTACCATATCTTAG	786
Db	788	TGTGTGTCAGATTTGGCAAGTCAAAATTTGGATGTGTTCTTTTACCATATCTTAG	842
RESULT 4			
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LOCUS	AL553333	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA	
DEFINITION	AL553333	clone GSD01075B08 5-PRIME. mRNA sequence.	
ACCESSION	AL553333		
VERSION	AL553333.3	GI:45859102	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
	On Feb 15, 2001 this sequence version replaced gi:31275147.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE		

Email: seq@genoscope.cns.fr Web: www.genoscope.cns.fr
The first strand cDNA was primed with a NotI-collod(CT) primer. Five prime
and enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1653.[†]

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdnas=CSD01075Dx04QPl&c=1653.r>.

FEATURES

SOURCE	1. .889
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/db_xref="caxon:9606"
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/notes="1st strand cDNA was primed with a NotI-clio (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	59.5%;	Score 756.6;	DB 1;	Length 889;
Best Local Similarity	99.0%;	Pred. No. 2.5e-205;		
Matches 767;	Conservative	4;	Mismatches 3;	Indels 1;
				Gaps 1

Qy	12	TCACCTGCGGGCAGCTGACCCGGACCGCCCGTGGGACCTTGAAAGGGGATCCCGGGC	71
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Db	13	TCATCTGSGGGCAGCTGACCCGGACCGCCCGTGGGACCTTGAAAGGGGATCCCGGGC	72
Qy	72	CCCCGCTCTCTCAGAGCTGTTTTCTTCATAATTAAGAACATGTGAAACATGATTCACACA	131
		:	
Db	73	CCCCGCTCTCTCAGAGCTGTTTTCTTCATAATTAAGAACATGTGAAACATGATTCACACA	132
Qy	132	TTAGCTGATCATGTGACGAGTGTCAACTGCTGTGCTTCTCTTTCCCTTGGCTACT	191
		:	
Db	133	TTAGCTGATCATGTGACGAGTGTCAACTGCTGTGCTTCTCTTTCCCTTGGCTACT	192
Qy	192	TGCTCCTTGGAAAAAACAATTGCGCTGACGTGTTACGTGACCTTACTGAACTCCACAT	251
		:	
Db	193	TGCTCCTTGGAAAAAACAATTGCGCTGACGTGTTACGTGACCTTACTGAACTCCACAT	252
Qy	252	TCTCCATTGAAGTTTCATACCTATGCTGTGCTGCATGCTGTGTTCTCCCTCAGACAT	311
		:	
Db	253	TCTCCATTGAAGTTTCATACCTATGCTGTGCTGCATGCTGTGTTCTCCCTCAGACAT	312
Qy	312	ATTTTGGCATCGTGTTCACACAGATGTGACCACTGCTCTATGGAATCTGAAAATGACAG	371
		:	
Db	313	ATTTTGGCATCGTGTTCACACAGATGTGACCACTGCTCTATGGAATCTGAAAATGACAG	372
Qy	372	ATGCTGGCAGTAGTGGAAACAGCTGATGAGGACCGCTGAGGGGTTTGGCCAG -TTTTCCC	430
		:	
Db	373	ATGCTGGCAGTAGTGGAAACAGCTGATGAGGACCGCTGAGGGGTTTGGCCAGTTTTCCC	432
Qy	431	AGACTCCACGCTTTTGGCATCAGGGGACGCTGATGGAACCTGTGGTTTGTGGAATGCACA	490
		:	
Db	433	AGACTCCACGCTTTTGGCATCAGGGGACGCTGATGGAACCTGTGGTTTGTGGAATGCACA	492
Qy	491	GTCTATCAAAATTATATAGATGTGGTAGTGTTPAAAGATGGCTCTTGGCGGCATGTGATT	550
		:	
Db	493	GTCTATCAAAATTATATAGATGTGGTAGTGTTPAAAGATGGCTCTTGGCGGCATGTGATT	552
Qy	551	TTCTCCTTAATGGAAGCTTCTTGTACAGTGGGCTCCCATGTGGGATTTAACAGTGGGGA	610
		:	
Db	553	TTCTCCTTAATGGAAGCTTCTTGTACAGTGGGCTCCCATGTGGGATTTAACAGTGGGGA	612
Qy	611	TGATAAAATAGAGGTGTCTGATAGTGAATAAAGCAGATGATCTTGGAATTAACCTGCTCGA	670
		:	
Db	613	TGATAAAATAGAGGTGTCTGATAGTGAATAAAGCAGATGATCTTGGAATTAACCTGCTCGA	672
Qy	671	TTTTTCTTCAACGCCAGTTTCTGATGGAACAAGGTCTTCAGTTTTTTTGGACTGGCATC	730
		:	

Db	673	TTTTTCTTCAAGCAGCATGTTCTGTATGTAGGAACAAGTCTTCAAGTTTTCAGCTGGACATC	733
Qy	731	ATGTGTCAGAGATTGCCCAATGCAATAATTGGATTGTTCTTTTACCATATCTTA	785
Db	733	ATGTGTCAGAGATTGCCCAAGTCAAAATTTGGATTGTTCTTTTACCATATCTTA	787
RESULT 5			
LOCUS	BMS43484		
DEFINITION	AGENCOURT 6492519 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726572		
ACCESSION	BMS43484		
VERSION	BMS43484.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1010)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LHAM12719 row: e column: 05 High quality sequence start: 6 High quality sequence stop: 669. Location/Qualifiers 1..1010 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5726572" /issue_type="hippocampus" /lab_host="DH10B" /clone_id="NIH_MGC_124" /note="Organ: brain; Vector: pCMV-SPORT6, site 1: EcoRV (destroyed); site 2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."		
FEATURES			
source			
ORIGIN			
Query Match	56.3%	Score 716.6;	DB 4; length 1010;
Best Local Similarity	97.6%;	Pred. No. 7.9e-194;	
Matches	760;	Conservative 0;	Mismatches 14; Indels 5; Gaps 3;
Qy	12	TCACCTGGGGGCGGACAGTACCCCGCACCCCGCGTGGGACCTTGAAGGCGGATCCGGCGG	71
Db	87	TCACCTGGGGGCGGACAGTACCCCGCACCCCGCGTGGGACCTTGAAGGCGGATCCGGCGG	146
Qy	72	CCCCGGCTCCGCGAGGCGTGTCTTTCTTCAAAATAAAGACATGGGAACGATTCACACACA	131
Db	147	CCCCGGCTCCGCGAGGCTGTCTTTCTTCAAAATAAAGACATGGGAACGATTCACACACA	206
Qy	132	TTAGCTGATCATGTGTGACGATGTCAACTGCTGTGCTTCTCTCTTTCCCTCTTGGCTACT	191
Db	207	TTAGCTGATCATGTGTGACGATGTCAACTGCTGTGCTTCTCTCTTTCCCTCTTGGCTACT	266
Qy	192	TGCTCTTGGACAAACAATTGCGCTGTACTCTGTACTGTAAGTACTTGAAGTAAGTGGACAT	251
Db	267	TGCTCTTGGACAAACAATTGCGCTGTACTCTGTACTGTAAGTACTTGAAGTAAGTGGACAT	326

Qy	252	TCACGATTTGAAGTTTCACTTACCTATGCGTCGTCACGTCGCTGTTTCTCCCTTCAGGACAT	311
Db	327	TCCTCATTTGAAGTTTCACTTACCTATGCGTCGTCACGTCGCTGTTTCTCCCTTCAGGACAT	386
Qy	312	ATTTTGGCAGTCGTTTCACAGATGGTAGCCACGTGCTCTATGAGATACTGAAAAATGACAG	371
Db	387	ATTTTGGCAGTCGTTTCACAGATGGTAGCCACGTGCTCTATGAGATACTGAAAAATGACAG	446
Qy	372	ATGTGGCAGTATGGAACGCTTAGTGGAGACCCCTGTAGGGTTCAGCTTTTCCCA	431
Db	447	ATGTGGCAGTATGGAACGCTTAGTGGAGACCCCTGTAGGGTTCAGCTTTTCCCA	506
Qy	432	GACGCCACGTTTGGCATCAGGGGCGACGTGANGGAATGAGTGGTTTGTGGAAATGCACAG	491
Db	507	GACGCCACGTTTGGCATCAGGGGCGACGTGANGGAATGAGTGGTTTGTGGAAATGCACAG	566
Qy	492	TCATACAAATTATATAGATGTGTAGTGTAAAGATGGCTTCCTTGGCGCATGTGCATTT	551
Db	567	TCATACAAATTATATAGATGTGTAGTGTAAAGATGGCTTCCTTGGCGCATGTGCATTT	626
Qy	552	TCCTCTAATGGAAGCTTCTTTGTACCTGCTCTCATGTGTGTATTTAACGTGTGGAT	611
Db	627	TCCTCTAATGGAAGCTTCTTTGTACCTGCTCTCATGTGTGTATTTAACGTGTGGAT	686
Qy	612	GATAAATGAGGTGTGCAATAGTAAAAAGCA-CATGATCTTGGAAATTAACCTCTGGCA	670
Db	687	GATAAATGAGGTGTGCAATAGTAAAAAGCAATGATTTGGAATTAACCTCTGGCA	746
Qy	671	TTTTTCTTCACAGCCATTTCTGATGAGAACAA--GGCTTCAGTTTTCAGTGGCA	728
Db	747	TTTTTCTTCACAGCCGTTCTGATGAGAACAAAGGCTTCAGTTTTCAGTGGCA	806
Qy	729	TCATGTGTCAGAGTTTCCCAAGTAAAA--TTTGAAATTTTCTTTAACCATATCTTA	785
Db	807	TCATGTGTCAGAGTTTTCAGTAAAAAATTTGAAATTTTCTTTAACCATATCTTA	865
RESULT 6			
LOCUS	BI603184	858 bp	linear
DEFINITION	60324982BF1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301559 5',		
ACCESSION	BI603184		
VERSION	BI603184.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 858)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rgs@bts-remail.nih.gov Tissue Procurement: Miklos Palokovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHRI), Shiroki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLNL at: http://image.llnl.gov Plate: LHAM1763 row: h column: 08 High quality sequence stop: 756. Location/Qualifiers 1..858 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5301559" /tissue_type="hypothalamus"		
FEATURES			
source			

Qy	312	ATTTGGCATGCTTTTCAACAGATGGATGACACTGCTGCATATGAAATACGAAATATGACAG	371
Dp	316	A-TTTGGCATGCTTTTCAACAGATGGATGACACTGCTGCATATGAAATACGAAATATGACAG	374
Qy	372	ATCTGGCAGTGTATGAAACACGCTTAGTGGACGCCCTGTGAGGGTTTGGCAGTTTCCCA	431
Dp	375	ATCTGGCAGTGTATGAAACACGCTTAGTGGACGCCCTGTGAGGGTTTGGCAGTTTCCCA	434
Qy	432	GACCTCCAGTGTGGGATCAGGGGACGCTATGGAACATGGTGTTTGTGGAAATGCACAG	491
Dp	435	GACCTCCAGTGTGGGATCAGGGGACGCTATGGAACATGGTGTTTGTGGAAATGCACAG	494
Qy	492	TCATACAAATTATATAGATGTGTAGTGTAAAGATGGCTCTTGGCCGACATGTGCATTT	551
Dp	495	TCATACAAATTATATAGATGTGTAGTGTAAAGATGGCTCTTGGCCGACATGTGCATTT	554
Qy	552	TTCTCTTAATGGAAGCTTCTTTGTCACTGGCTCTTC-ATGTGTGATTTAAACAGTGTGGGA	610
Dp	555	TTCTCTTAATGGAAGCTTCTTTGTCACTGGCTCTTCMAATGTGGTGAATTTAAACAGTGTGGGA	614
Qy	611	TGATAAATAGAGTGTCTGCATAGTGA-AAAAGCATGATCTTGGAAATTAAC- TGCTGC	668
Dp	615	TGATAAATAGAGTGTCTGCATAGTGAATAAAGCATGATCTTGGAAATTAACCTTGCTGC	674
Qy	669	GATTTTCTTCAACGCCAGTTTC-TGATGAGAAACAAGTCTTCAgTTTTTTCGAC-TGG	726
Dp	675	GATTTTCTTCAACGCCAGTTTCTTGAATGGAGAACMAAGTCTTCAgTTTTTTCGACCTGG	734
Qy	727	CATCATGT-GGTCAAGATTGCCAAGTCAA- AATTGGATTTGTTCTTTTAACCAAAT	781
Dp	735	CATCATGTGGGTCAAGATTGGAGATGTCAACAATTTTGAAGCTGTACTTTTAACCAAAT	791

LOCUS	RESULT 8
CN793033	CN793033
DEFINITION	41279930 BARC 8BOV Bos taurus cDNA clone 8BOV_46H02 5', mRNA
ACCESSION	sequence.
VERSION	CN793033
KEYWORDS	CN793033.1 GI:47689013
SOURCE	EST.
ORGANISM	Bos taurus (cow)
	Bos taurus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE	1 (bases 1 to 728)
AUTHORS	Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and Matukumalli,L.K.
TITLE	Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL	Unpublished (2004)
COMMENT	Contact: Richard G. Baumann Bovine Functional Genomics Lab AKRI BLDG 162: BARC-East, Beltsville, MD 20705, USA Tel: 3015048604 Fax: 3015048744 Email: rbaumann@arri.barc.usda.gov Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt ' ' -trim fastavector identified by cross_match using options -mismatch 12 -minscore 12 Plate: 46 row: H column: 02 Seq primer: CCTATTTAGGTGACACTCTATGACAC High quality sequence stop:728.

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FEATURES
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location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_46H02"
/sex="female"

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/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH108_Tona"
/clone_id="BARC_8BOV"
/note="Organ: Intestine; Vector: PCWMSport6.1, Site_1:
Not1, Site_2: EcoRI; Normalized cow cDNA intestinal
library in PCWMSport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

```

[illegible]

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 505)
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strunberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 421.
FEATURES	Location/Qualifiers
SOURCE	1..505 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1722702" /dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares_placenta_8to9weeks_2NHPhc09" /note="Organ: placenta; Vector: pTR73 (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCATCTGAAGTGGAGCGCGCCGATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia) digested with Not I and cloned into the Not I and Eco RI sites of a modified pTR73 vector (pharmacia). Library constructed by Bento Soares and M.Fatima Bonaudo."
ORIGIN	
Query Match	38.8%; Score 493; DB 1; Length 505;
Best Local Similarity	99.8%; Pred. No. 9.1e-130; Indels 1; Gaps 1;
Matches 504; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	96 CTTCAATAAAGAACATGATGAACTGATTCACACATTAGTGATCATGTGACGATGTC 155
Db	1 CTTCAATAAAGAACATGATGAACTGATTCACACATTAGTGATCATGTGACGATGTC 60
QY	156 AACTGCTGTGCTTCTCTCTTCTCCCTCTGCTGCTACTTGCTCCTTGGAACAAACATTGGC 215
Db	61 AACTGCTGTGCTTCTCTCTTCTCCCTCTGCTGCTACTTGCTCCTTGGAACAAACATTGGC 120
QY	216 CTGTACTGTTACGATCTTACTGAACTGCACATCTTCATTGAACTTCAATCTAT 275
Db	121 CTGTACTGTTACGATCTTACTGAACTGCACATCTTCATTGAACTTCAATCTAT 180
QY	276 GCTGTCCACTGCTGCTGTTTCTCCCTTCAGGACATATTTTGGCATGCTGTTCAACAGAT 335
Db	181 GCTGTCCACTGCTGCTGTTTCTCCCTTCAGGACATATTTTGGCATGCTGTTCAACAGAT 240
QY	336 GGTAACCACTGCTCTATGGAATACTGAATAAGACAGATGCTGGCAGTATGGAACAGCT 395
Db	241 GGTAACCACTGCTCTATGGAATACTGAATAAGACAGATGCTGGCAGTATGGAACAGCT 300
QY	396 AGTGGACAGCCCTGTGAGGGTTTCCAGTTTTTCCCGAATCCAGCTGTTTGGCATCAGG 455
Db	301 AGTGGACAGCCCTGTGAGGGTTTCCAGTTTTTCCCGAATCCAGCTGTTTGGCATCAGG 360
QY	456 GCAGCTGATGGAACGTGCG -TTTGTGGAAGACACAGTCATACAAATTATATAGATCG 514
Db	361 GCAGCTGATGGAACGTGCGTTTGTGGAAGACACAGTCATACAAATTATATAGATCG 420
QY	515 TAGGTATTAAGATGGCTCTTGCGCGCATGTGCATTTTCTCTAATGGAAGCTTTTGT 574
Db	421 TAGGTATTAAGATGGCTCTTGCGCGCATGTGCATTTTCTCTAATGGAAGCTTTTGT 480
QY	575 CACTGGCTCTCATATGTGATTTA 599

Db	481	CACGCGCTCCTCATGTCGTATTTA	505
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LOCUS	BX282729	499 bp	mRNA linear EST 04-MAR-2003
DEFINITION	BX282729 NIH_MGC_116 Homo sapiens cDNA clone IMAGE9802211467 ;		
ACCESSION	IMAGE:5187309, mRNA sequence.		
VERSION	BX282729		
KEYWORDS	BX282729.1 GI:28615370		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 499) Ebert,L., Hell,O., Hennig,S., Neubort,P., Patzsch,E., Peters,M., Radehof,U., Schneider,D. and Korn,B.		
TITLE	Human Unigeneset - RZPD3		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGE9802211467. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libno=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M3u, primer sequence: CGTTGTAACACAGCGCCAGT.		
FEATURES	Location/Qualifiers		
SOURCE	1. 499 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE9802211467 ; IMAGE:5187309" /lab_host="DH10B" /clone_lib="NIH_MGC_116" /note="Organ: pooled colon, kidney, stomach; Vector: pCMW-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed) ; RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is: oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	38.2% ;	Score 486.2 ;	DB 5 ; Length 499 ;
Best Local Similarity	99.4% ;	Pred. No. 8.1e-128 ;	
Matches 488 ;	Conservative 0 ;	Mismatches 3 ;	Indels 0 ; Gaps 0 ;
Oy	296	CTCCCTCAGGACATATTTTGGATGATGTTCAACAGATGTATCACTGTCATATGAA	355
Db	1	CGCTCTGCGAGACATATTTTGGATGATGTTCAACAGATGTATCACTGTCATATGAA	60
Oy	356	TACTGAATAATGACAGATGCTGGAGATGATGAACAGCCTATGTGCAGCCCTGTGAGGT	415
Db	61	TACTGAATAATGACAGATGCTGGAGATGATGAACAGCCTATGTGCAGCCCTGTGAGGT	120
Oy	416	TTCGCAATTTTCCCAACATCCACGCTTTGGATCATAGGGGACGCTGATGAACTGTGCT	475
Db	121	TTCGCAATTTTCCCAACATCCACGCTTTGGATCATAGGGGACGCTGATGAACTGTGCT	180

QY 476 TTGTGGAATGCACAGTCATACAAATTATATAGATGTGTAAAGATGCTCCTT 535
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 Db 181 TTGTGGAATGCACAGTCATACAAATTATATAGATGTGTAAAGATGCTCCTT 240
 QY 536 GGGGGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTCTCATGTGTGA 595
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 Db 241 GGGGGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTCTCATGTGTGA 300
 QY 596 TTTAACAGTGTGGGATATAAATGAGGTCTGTCATATGAAAAAGACATGATCTTGG 655
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 Db 301 TTTAACAGTGTGGGATATAAATGAGGTCTGTCATATGAAAAAGACATGATCTTGG 360
 QY 656 AATTACCTGTGCGATTTTCTTCAAGCCAGTTTGTATGAGAACAAAGCTCTTCAGTT 715
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 Db 361 AATTACCTGTGCGATTTTCTTCAAGCCAGTTTGTATGAGAACAAAGCTCTTCAGTT 420
 QY 716 TTTTCGACTGGCATCATGTGTGTCAGATTGCGCAAGTCAAAATTGGATTGTTCTTTAC 775
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 Db 421 TTTTCGACTGGCATCATGTGTGTCAGATTGCGCAAGTCAAAATTGGATTGTTCTTTAC 480
 QY 776 CCATATCTTAG 786
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 Db 481 CCATATCTTAG 491

RESULT 11
 LOCUS B1759505 696 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603046888F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187309 5',
 mRNA sequence.
 ACCESSION B1759505
 VERSION B1759505.1 GI:15751083
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 696)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.lnl.gov
 Plate: LMNL1467 row: 0 column: 22
 High quality sequence stop: 696.
 Location/Qualifiers
 1. 696

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 /note="Organ: pooled colon, kidney, stomach; Vector:
 PCWV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 clones, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."

Query Match 38.2%; Score 486.2; DB 4; Length 696;
 Best Local Similarity 99.4%; Pred. No. 9, 1e-128;
 Matches 486; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 296 CTCCTCTTCAGGACATATTTTGGCATGCTGTTCAACAGATGTAACCATGCTATGAA 355
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 Db 1 CGCTCTGCAGAGCATATTTTGGCATGCTGTTCAACAGATGTAACCATGCTATGAA 60
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 Db 61 TACTGAAATGAGACAGATGCTGGCAGATGAGAACACCTTAGTGGCAGCCCTGAGAGGT 120
 QY 416 TTGCCAGTTTCCCAACTCCAAGTGTGGCATCAGGGCAGCTGATGAACTGTGT 475
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 Db 121 TTGCCAGTTTCCCAACTCCAAGTGTGGCATCAGGGCAGCTGATGAACTGTGT 180
 QY 476 TTGTGGAATGCACAGTCATACAAATTATATAGATGTGTAAAGATGCTCCTT 535
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 Db 181 TTGTGGAATGCACAGTCATACAAATTATATAGATGTGTAAAGATGCTCCTT 240
 QY 536 GGGGGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTCTCATGTGTGA 595
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 Db 241 GGGGGCATGTGCATTTTCTCTTAATGGAAGCTTTTGTCACTGGCTCTCATGTGTGA 300
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 Db 301 TTTAACAGTGTGGGATATAAATGAGGTCTGTCATATGAAAAAGACATGATCTTGG 360
 QY 656 AATTACCTGTGCGATTTTCTTCAAGCCAGTTTGTATGAGAACAAAGCTCTTCAGTT 715
 |||||
 Db 361 AATTACCTGTGCGATTTTCTTCAAGCCAGTTTGTATGAGAACAAAGCTCTTCAGTT 420
 QY 716 TTTTCGACTGGCATCATGTGTGTCAGATTGCGCAAGTCAAAATTGGATTGTTCTTTAC 775
 |||||
 Db 421 TTTTCGACTGGCATCATGTGTGTCAGATTGCGCAAGTCAAAATTGGATTGTTCTTTAC 480
 QY 776 CCATATCTTAG 786
 |||||
 Db 481 CCATATCTTAG 491

RESULT 12
 LOCUS AK011391 2027 bp mRNA linear HTC 03-APR-2004
 DEFINITION Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
 enriched library, clone:2610014F08 product:hypothetical SAM domain
 (sterile alpha motif)/Modified RING finger domain/G-protein beta
 WP-40 repeats containing protein, full insert sequence.
 ACCESSION AK011391
 VERSION AK011391.1 GI:12847483
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 REFERENCES
 1 Carninci, P. and Hayashizaki, Y.
 Title High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 REFERENCES
 1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Title Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 20499374
 3
 REFERENCES
 1 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Qy 787 ----- 786
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Db 911 ATGGAAGAATGCTTGCATCGGGGTCACTGGATAAATCTGTATCATATACATGATCGGCC 970
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Qy 787 ----- 786
Db 1031 CACCCAACTCTCTTACTGCTAATGCTGTCTAATGACCAAGACAGTGAACATTTGGCAGT 1090
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Db 1091 TTGACCTGGAACACCTTGGCCAAAGACATGAAAGACCCGCTGAAACATTTTCACTGAG 1150
Qy 826 ATTGTCAGAGAGAGTCTCTCAACATGCTTTGTGCAACAATTTAAAGATCTTGTG 885
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Qy 946 TGGCTGATGATTTGAAATGTAATCTCTAGAGCTGCTGTAAGATGCTGAGAAATTTG 1005
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Qy 1006 AAGAGCTCAGAGACCAAGTTAAATCCCTTCTTCAAGAAATCTGATGAATTTATGTC 1065
Db 1331 AAGAGCTCAGAGACCAAGTTAAATCCCTTCTTCAAGAAATCTGATGAATTTATGTC 1390
Qy 1066 CAATTAAGTGAAGAACTTATGAAGAAATCCGCTGATGCTGATGAGTCTTATCATATGAA 1125
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RESULT 13
CN407189 463 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600054632 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN407189
VERSION CN407189.1 GI:47394734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, Y., Xu, C., Fang, R., Wei, H., Zhang, S., Lei, S., Murag, J., Fisk, G.J.,
Lebkowsky, J. and Stanton, L.W.
TITLE Transcriptional characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R

Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 463 Std Error: 0.00.
Location/Qualifiers
1..463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_id="GRN_PREHEP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated h9s cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.6e-121;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 CTGCGGCGACGAGACCCGACCCGCTGAGCACTTGAAGGGGATCCCGCGCCC 75
Db 1 CTGCGGCGACGAGACCCGACCCGCTGAGCACTTGAAGGGGATCCCGCGCCC 60
Qy 76 CGCTCTCAGAGCTGTTTTCTTCAATTAAGAAACATGTTGAATCTACACATTAG 135
Db 61 CGCTCTCAGAGCTGTTTTCTTCAATTAAGAAACATGTTGAATCTACACATTAG 120
Qy 136 CTGATCATGCTGACAGATGTAACCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 195
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Qy 196 CTTTGAACAAACAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
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Qy 256 CATTGAATTTCAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
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Db 301 TGGCATGCTGTTCAACAGATGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 376 TGGCAGTGAAGAAACAGCTAGTGGAGCCCTGGAAGGTTTGGCAGTTTCCCGAGACT 435
Db 361 TGGCAGTGAAGAAACAGCTAGTGGAGCCCTGGAAGGTTTGGCAGTTTCCCGAGACT 420
Qy 436 CCAAGTGTGTTGTCATCAGGGGCACTGATGAACTGTGTTTT 478
Db 421 CCAAGTGTGTTGTCATCAGGGGCACTGATGAACTGTGTTTT 463

RESULT 14
AL533462 967 bp mRNA linear EST 24-MAR-2004
LOCUS AL533462/c
DEFINITION AL533462 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN004YJ15 3-PRIME, mRNA sequence.
ACCESSION AL533462
VERSION AL533462.2 GI:31260543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

Db	420	TAGCTCATTGGAGGCTGTGGCTTTTTCGCCATGGAGGCGCTTTGTCACTGCGTCTTC	479
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Qy	647	TGATCTTGGAAATTACCTCTGCGGATTTTTTCTCACAGCCAGTTTCTGATGAGAAACAAG	706
Db	540	CGATCTGGGATCACTCTGCTGACGCTTTTCTCACAGCCTCTCTCTGCGGGAG--AAAG	596
Qy	707	TCTTCAGTTTTTTTCAGCTGCGATCAATGTGTGTCAGGATTCGCAAGTCAAAATTTGATTTG	766
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Qy	767	TTCTTTTACCATACTTA	785
Db	657	TACTATTACCGTGTCTTA	675

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:28:45 : Search time 178 Seconds
(without alignments)
11692.944 Million cell updates/sec

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1272
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Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813839 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfilest.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	49.6	3.9	7218	1	US-08-232-463-14
3	45.8	3.6	7218	1	US-08-232-463-14
4	44.8	3.5	1221	3	US-08-965-600-2
5	44.8	3.5	1221	3	US-09-489-506-2
6	43.8	3.4	1141	4	US-09-806-708B-22
7	43.6	3.4	1141	4	US-09-806-708B-22
8	43.6	3.4	937	4	US-10-101-464A-251
9	40.4	3.2	162450	3	US-09-345-882-1
10	40	3.1	2152	1	US-08-188-582-17
11	40	3.1	2152	1	US-08-646-715-17
12	40	3.1	246240	2	US-08-724-394A-20
13	40	3.1	246240	2	US-08-724-394A-21
14	40	3.1	246240	2	US-08-724-394A-22
15	39.6	3.1	5152	3	US-09-690-364-10
16	39.6	3.1	1664976	4	US-08-916-421B-1
17	39.6	3.1	1664976	4	US-09-692-570-1
18	38.2	3.0	2085	2	US-08-283-917-8
19	38.2	3.0	2085	2	US-08-961-716-8
20	38	3.0	2142	4	US-09-614-221A-331
21	37.8	3.0	601	4	US-09-949-016-138114
22	37.8	3.0	601	4	US-09-949-016-138115
23	37.8	3.0	601	4	US-09-949-016-138116
24	37.8	3.0	112705	4	US-09-949-016-138116
25	37.6	3.0	1464	4	US-09-248-796A-1960
26	37.4	2.9	29357	4	US-09-949-016-16676
27	37	2.9	732	4	US-09-248-796A-2341

28	36.8	2.9	1611	3	US-09-302-769-13	Sequence 13, Appl
29	36.6	2.9	3127	4	US-09-710-279-3502	Sequence 3502, Ap
30	36.6	2.9	6968	4	US-09-710-279-759	Sequence 759, Ap
31	36.6	2.9	7215	3	US-09-134-001C-627	Sequence 627, Appl
32	36.4	2.9	3081	4	US-09-949-016-2486	Sequence 2486, Ap
33	36.2	2.8	1566	4	US-09-248-796A-9260	Sequence 9260, Ap
34	35.8	2.8	389	4	US-09-270-767-26536	Sequence 26536, A
35	35.8	2.8	832	4	US-09-621-976-2813	Sequence 2813, Ap
36	35.8	2.8	899	4	US-09-270-767-11026	Sequence 11026, A
37	35.8	2.8	1743	4	US-09-248-796A-11015	Sequence 11015, A
38	35.6	2.8	1182	4	US-09-248-796A-4568	Sequence 4568, Ap
39	35.6	2.8	4892	4	US-09-976-594-167	Sequence 167, Appl
40	35.6	2.8	5158	4	US-09-023-655-1347	Sequence 1347, Ap
41	35.6	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
42	35.6	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
43	35.4	2.8	2417	4	US-09-254-776B-3	Sequence 3, Appli
44	35.4	2.8	3747	3	US-09-690-364-17	Sequence 17, Appl
45	35.4	2.8	7028	4	US-09-949-016-4194	Sequence 4194, Ap

ALIGNMENTS

RESULT 1
US-09-620-312D-768
Sequence 768, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Ruihong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinphast
APPLICANT: Dymnac, Radote T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PE FL_genes Version 1.0
SEQ ID NO 768
LENGTH: 1844
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (164)..(1594)
US-09-620-312D-768

Query Match 75.8%, Score 964.2, DB 4, Length 1844;
Best Local Similarity 81.8%, Pred. No. 1.9e-307;
Matches 1252, Conservative 3, Mismatches 3, Indels 276, Gaps 1.

DB 65 TCACCTGGCGGCGACGTCGACCGCCCGTGGGCACTTGAAGCGCATCCCGCGG 71
12 TCACCTGGCGGCGACGTCGACCGCCCGTGGGCACTTGAAGCGCATCCCGCGG 71
65 TCACCTGGCGGCGACGTCGACCGCCCGTGGGCACTTGAAGCGCATCCCGCGG 124

QY	72	CCCCGGCTCCTCAGAGCTCTTTTCTTCAAAATTAAGAAATGGGTGAACGATTTCAACA	133
Db	125	CCCCGGCTCCTCAGAGCTCTTTTCTTCAAAATTAAGAAATGGGTGAACGATTTCAACA	184
QY	132	TTAGCTGATCATGTGACGATGTCAACTGCTGTGCTCTTTCCTTTTCCCTTTGGGTACT	191
Db	185	TTAGCTGATCATGTGACGATGTCAACTGCTGTGCTCTTTCCTTTTCCCTTTGGGTACT	244
QY	192	TGCTCCTTGGACAAAACAATTGGCCGTGATCTGGTTAAGTGAACCTTATCTGAACGCCAAT	251
Db	245	TGCTCCTTGGACAAAACAATTGGCCGTGATCTGGTTAAGTGAACCTTATCTGAACGCCAAT	304
QY	252	TCTCCATTGAAAGTTTCATACCTATGCTGTCCACTGCTGCTGTTTCTCCCTTCAGACAAT	311
Db	305	TCTCCATTGAAAGTTTCATACCTATGCTGTCCACTGCTGCTGTTTCTCCCTTCAGACAAT	364
QY	312	ATTTTGGCATTCGTGTTCAACACATGGTACCACTGTCTTATGAAATACTGAAAAATGACACG	371
Db	365	ATTTTGGCATTCGTGTTCAACACATGGTACCACTGTCTTATGAAATACTGAAAAATGACACG	424
QY	372	ATGCTGGCAGTATGAGAACAGCCTTAATGGCAGCCCTGTGAGGGTTTGGCCAGTTTCCCA	431
Db	425	ATGCTGGCAGTATGAGAACAGCCTTAATGGCAGCCCTGTGAGGGTTTGGCCAGTTTCCCA	484
QY	432	GACTCCACGTGTTTGGCATCAGGGGCACTGATGAACTGTGTGTTTGTGGAATGACACG	491
Db	485	GACTCCACGTGTTTGGCATCAGGGGCACTGATGAACTGTGTGTTTGTGGAATGACACG	544
QY	492	TCATCAAAATTAATGATGTGTGATGTATAAGATGGCTCCTTGGCCGGCATGTGCATT	551
Db	545	TCATCAAAATTAATGATGTGTGATGTATAAGATGGCTCCTTGGCCGGCATGTGCATT	604
QY	552	TCTCCTAATGAGAGCTTCTTTGTCACTGCTCCTCATGTGTGTGATTTAAACAGTGTGGAT	611
Db	605	TCTCCTAATGAGAGCTTCTTTGTCACTGCTCCTCATGTGTGTGATTTAAACAGTGTGGAT	664
QY	612	GATAAAATGAGGTGTCTGATAGTGA AAAAGCAATGATCTTGGATTAACCTGCTGGAT	671
Db	665	GATAAAATGAGGTGTCTGATAGTGA AAAAGCAATGATCTTGGATTAACCTGCTGGAT	724
QY	672	TTTTCTTCAACAGCAGTTTCTGATGAGAAACAAGTCTTCAGTTTTCGACTGGCATCA	731
Db	725	TTTTCTTCAACAGCAGTTTCTGATGAGAAACAAGTCTTCAGTTTTCGACTGGCATCA	784
QY	732	TGTGTCAAGATTTGCCCAATCAAAATTTGATTTGTTCTTTTACCATAATCTT-----	784
Db	785	TGTGTCAAGATTTGCCCAATCAAAATTTGATTTGTTCTTTTACCATAATCTT-----	844
QY	785	-----	784
Db	845	GAAATTAATAATTAAGATACACTGAGTGGGCACTGTGCTCTGTCTGGCTGTGCTTT	904
QY	785	-----	784
Db	905	TCCCATGATGGCAGATGCTAGTCTCAGGGTCAATGATTAAGTCTGTCAATGATATGAT	964
QY	785	-----	784
Db	965	ACTAATACTGAGAATTAATCTTACACACTTGACTCAGACACACAGGTAATGACAACTTGT	102
QY	785	-----	784
Db	1025	GCTTTTGACATAATACCTTTTACTTGTCTAGTGTCAATGACAAAACAGTGAACATC	108
QY	785	-----AGCAAGCGCACAGAAATCAGCTGAAGCAA	815
Db	1085	TGGCAATTTGACCTGGAACAATCTTTGCCAAGCAGAGAGCACAGAAATACAGCTGAAGCAA	114
QY	816	TTTACCGAAGATTTGGTCAAGAGAGTGTCTCAACATGGCTTTGTGTCACACAAGATTTAAAA	875
Db	1145	TTTACCGAAGATTTGGTCAAGAGAGTGTCTCAACATGGCTTTGTGTCACACAAGATTTAAAA	120
QY	876	GATCTTTGTGGTAATTTTCAAGATGAATAACATTTGATGAAAAAGACTGTTGAATCTTACA	935

Db	1205	GATTTTGTGGTATTTTTCAGATGCAATACATTGATGGAAGAAAGCTGTGAATCTTACA	1264
Qy	936	AAGAANGTCGCGCTGATGATTTGAAAATTGAATCTCTAGACTGCGTAGTAAAGTCCTG	995
Db	1265	AAAGAAAAGTCGTGGTGTATGATTTGAAAATTGAATCTCTAGAGACTGCGTAGTAAAGTCCTG	1324
Qy	996	AGGAAAATTGGAAGAGCTCAGAGACCAAGGTTAAATCCCTTCTTCAGGAATTCCGTGATGAA	1055
Db	1325	AGGAAAATTGGAAGAGCTCAGAGACCAAGGTTAAATCCCTTCTTCAGGAATTCCGTGATGAA	1384
Qy	1056	TTTATATGTCCAATTAAGTATGAGAACTTATGAAAGATCCGTCATTCGATCAGATGCGTAT	1115
Db	1385	TTTATATGTCCAATTAAGTATGAGAACTTATGAAAGATCCGTCATTCGATCAGATGCGTAT	1444
Qy	1116	TCATATGAAAAAGGAAGCAATGCAAAATTGATGACGAAAAAGAAAGCTACAAATGCCATG	1175
Db	1445	TCATATGAAAAAGGAAGCAATGCAAAATTGATGACGAAAAAGAAAGCTACAAATGCCATG	1504
Qy	1176	ACAAATCTGTCTTCTTCCCTTCAGGCGTACTTACACCAATAGACTGTAATAATGCCATC	1235
Db	1505	ACAAATCTGTCTTCTTCCCTTCAGGCGTACTTACACCAATAGACTGTAATAATGCCATC	1564
Qy	1236	AATGATGCGCTGAGACACACCAAAAGTAAA	1266
Db	1565	AATGATGCGCTGAGACACCAAAAGTAAA	1595
RESULT 2			
US-08-232-463-14			
Sequence 14, Application US/08232463			
Patent No. 5670367			
GENERAL INFORMATION:			
APPLICANT: DORNER, F.			
APPLICANT: SCHEIFLINGER, F.			
APPLICANT: FALKNER, F. G.			
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS			
NUMBER OF SEQUENCES: 52			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Foley & Lardner			
STREET: 1800 Diagonal Road, Suite 500			
CITY: Alexandria			
STATE: VA			
COUNTRY: USA			
ZIP: 22313-0299			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/232.463			
FILING DATE:			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/07/935.313			
FILING DATE:			
APPLICATION NUMBER: EP 91 114 300.6			
FILING DATE: 26-AUG-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: BENT, Stephen A.			
REGISTRATION NUMBER: 29,768			
REFERENCE/DOCKET NUMBER: 30472/114 IMMU			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (703)836-9300			
TELEFAX: (703)683-4109			
TELEX: 899149			
INFORMATION FOR SEQ ID NO: 14:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 7218 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			

IMMEDIATE SOURCE:
CLONE: PTZgpc-Fls
US-08-232-463-14

Query Match 3.9%; Score 49.6; DB 1; Length 7218;
Best Local Similarity 8.3%; Pred. No. 0.0001;
Matches 34; Conservative 200; Mismatches 174; Indels 0; Gaps 0;

QY 4 TTGGCTTACCTGCGGCGACGTGACCCGCGGCGGACCTTAAGACCGGAT 63
DB 1102 YY 1161
QY 64 CCGCGCGCGCGCGCGCTGCGACGCTGTTTCTTCAATAAGAACGTGAACCTGA 123
DB 1162 YY 1221
QY 124 TTCACATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 183
DB 1222 YY 1281
QY 184 TGCGTACTGCTCTTGACAAACAATGCGCTGCTGCTGCTGCTGCTGCTGCT 243
DB 1282 YY 1341
QY 244 TGCCACATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
DB 1342 YY 1401
QY 304 CAGACATATTTTGGCATCGTGTCAACAGATGATGATGATGATGATGATGAT 363
DB 1402 YY 1461
QY 364 ATGACAGATGCTGCGACGTGATGACAGCTGATGATGATGATGATGATGAT 411
DB 1462 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509

RESULT 3

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
STATE: Alexandria
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpc-Fls
US-08-232-463-14

Query Match 3.6%; Score 45.8; DB 1; Length 7218;
Best Local Similarity 9.8%; Pred. No. 0.0018;
Matches 47; Conservative 215; Mismatches 217; Indels 0; Gaps 0;

QY 686 AGTTCTGATGAGAACAGAGTCTTCAAGTATGATGATGATGATGATGATGAT 745
DB 1539 AGCATGCTCTAGACCATCTATGCTTCAAAAACGCGATGATGATGATGAT 1480
QY 746 CCAAGTCAAAATTTGATGTTCTTTTACCATATCTTGAAGGCGCACAGACATCA 805
DB 1479 TTACCTATCTATGCAAGTATGATGATGATGATGATGATGATGATGATGAT 1420
QY 806 GCTGACCAATTTACCAAGATGCTGAGAGAGTGTCTCAACATGCGCTTGTGACA 865
DB 1419 RRR 1360
QY 866 AGATTAAAGATCTTGTGATTTTCAAGATCAATGATGATGATGATGATGATGAT 925
DB 1359 RRR 1300
QY 926 GAATCTTCAAAAAGAAAGTGGCTGATGATTTGAATGATCTTAGACGCTAG 985
DB 1299 RRR 1240
QY 986 TAAAGTCTGAGAAATTAAGAGCTCAGAGCCAGCAAGTTAAATCCCTTCTTAGAGAT 1045
DB 1239 RRR 1180
QY 1046 TCCGTGATGATTTATGATCAATTAAGTATGATGATGATGATGATGATGATGAT 1105
DB 1179 RRR 1120
QY 1106 AGATGCTATTCATATGAAAGAGCAATGATGATGATGATGATGATGATGATGAT 1164
DB 1119 RRR 1061

RESULT 4

US-08-965-600-2
Sequence 2, Application US/08965600
Patent No. 6077688

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Puri
TITLE OF INVENTION: NEW TRANSDUCIN BETA-1 SUBUNIT
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,600
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0416 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 194046
; US-08-965-600-2

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Query Match          3.5%; Score 44.8; DB 3; Length 1221;
Best Local Similarity 49.3%; Pred. No. 0.0011;
Matches 146; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

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QY 328 CAACAGATGTACCTGCTCTATGGAATCTGAAAATGACAGATGCTGGCAGTATGG 387
DB 579 CCATAGATGGAATCATCATATTTTATGATGCACTGGAATACTCTGCATATCCCTGG 638
QY 388 AACAGCTATGAGAGCCCTGTAGGGTTTGCCAGTTTCCCAAGTCCACGTGTTGG 447
DB 639 AAGGCC---ATGCCATGCCCATTTGCTCTGACCTTTTCCCGGACTCCGACTCCTTG 695
QY 448 CATCAGGGGAGCTGATGAACTGTGTTTGTGGAATGCAAGTCAATACAAATTATATA 507
DB 696 TCACCTCTTCAAGATGAGCTCTACATCAAGATCTATGATGACAAAGCCAAATTTGGCTG 755
QY 508 GATGTGATGTGTTAAAGATGCTCTCTGGCGGCAATGCAATTTCTCTTAATGGAAGCT 567
DB 756 GCACGCTGAGCGGCGCATGCTCTCTGGGTGCTGAACGTTGCAATTCCTCGATGACACTC 815
QY 568 TCTTTGCTACGTGCTCTCATGTGATTTAAACAGTGGGATGAATAAATGAGG 623
DB 816 ACTTTGTTCCAGTTGCTCTGACAAAAGTGTAAAGTTGGAGTTGGAACGAGG 871

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RESULT 5

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US-09-489-506-2
; Sequence 2, Application US/09489506
; Patent No. 6465619
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW TRANSDUCIN BETA-1 SUBUNIT
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,506
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,600
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0416 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 194046
; US-09-489-506-2

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Query Match          3.5%; Score 44.8; DB 3; Length 1221;
Best Local Similarity 49.3%; Pred. No. 0.0011;
Matches 146; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

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QY 328 CAACAGATGTACCTGCTCTATGGAATCTGAAAATGACAGATGCTGGCAGTATGG 387
DB 579 CCATAGATGGAATCATCATATTTTATGATGCACTGGAATACTCTGCATATCCCTGG 638
QY 388 AACAGCTATGAGAGCCCTGTAGGGTTTGCCAGTTTCCCAAGTCCACGTGTTGG 447
DB 639 AAGGCC---ATGCCATGCCCATTTGCTCTGACCTTTTCCCGGACTCCGACTCCTTG 695
QY 448 CATCAGGGGAGCTGATGAACTGTGTTTGTGGAATGCAAGTCAATACAAATTATATA 507
DB 696 TCACCTCTTCAAGATGAGCTCTACATCAAGATCTATGATGACAAAGCCAAATTTGGCTG 755
QY 508 GATGTGATGTGTTAAAGATGCTCTCTGGCGGCAATGCAATTTCTCTTAATGGAAGCT 567
DB 756 GCACGCTGAGCGGCGCATGCTCTCTGGGTGCTGAACGTTGCAATTCCTCGATGACACTC 815
QY 568 TCTTTGCTACGTGCTCTCATGTGATTTAAACAGTGGGATGAATAAATGAGG 623
DB 816 ACTTTGTTCCAGTTGCTCTGACAAAAGTGTAAAGTTGGAGTTGGAACGAGG 871

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RESULT 6

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US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Placenta
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)

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OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 3.4%, Score 43.8, DB 4, Length 1141;
Best Local Similarity 9.6%; Pred. No. 0.0023;
Matches 67; Conservative 279; Mismatches 341; Indels 9; Gaps 1;

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538 CGGATGCGATTTCTCTCTAATGAGCTCTTTGTCAGTGGTCCCATGCTGAT 597
53 MSKRKMTTAMTKKRYWNNKSRWMMGMYKKWYBDAANTSBKTHARRKMDKTAYBM 112
598 TAACAGTGGGATGATATAATGAGTGTCTGATAGTGAAGAAAGACATGCTGGAA 657
113 TMTKMKCTGGRHRYWYBAMVDVYDHHYVYANNNATMTGCMXDXDRTHMMKKNNNA 172
658 TTACTGCTGGATTTTCTTCAACAGCCAGTTTGTATGAGAAAGAGCTTCAAGTTT 717
173 TGMDDTKYHMMNNNGCBTVTMVRYKTRDMSBKRMNYGMBWMKMSYDVYVWVWDD 232
718 TTGACGCGCATCTGTGTCAGATTCGCAAGTCAAAATTTGATGTTCTTTACC 777
233 MCKKRVKRWFT-----RGRMYVYVAMBTAHRRYNNNGTBAVAYRRWTTNNNN 283
778 ATATCTTAGCAGGCGCAGACAGATCAGTGAAGCAATTTACCGAAGTTGTCAGAG 837
284 NAKMCKRAKYWGNRABVNSTCTTKWSKITKVRTSCANNCRAGDANKHKMKMSAAM 343
838 AGTGCTCTCAACATGCTGTTGTCACAAAGATTTAAAGATCTGTGTGATTTTCAAG 897
344 GYVNNNNNNNNMTYKKARHBAWDMVMSAWKKHANAAYSRKKMTBKSKTWNNG 403
898 TGAATTAATGATGAGAAAGACTGTTGATCTTCAAAAGAAAGCTGCTGATGATT 957
404 TTMKRMWAMWKMMDMBGTYNNNNNGRTYTGTTKXKKMTYTKMVAANCKRADMCK 463
958 TGAATTAATGATCTCTAGAGCTGCTAGTAAAGTCTGAGAAAGTGAAGCTCAGGA 1017
464 TCTNNNTTMMCKTYNNNNCYKSMTNGSKHBAAVYVWMMRRVHAANNMMWDYMK 523
1018 CCAAGTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTATATGTCATTAAG 1077
524 ACTYKKBVCSKMMNNNYAAMWTKSWMYTSRYWKTNNNSRWRSDTFSMGRANNYAB 583
1078 AACTATGAAGAAGATCCGCTATCCATGATGCGATGCTATTCATATGAAGAAGCAATCG 1137
584 HYGTMTTMBWBSHTBHBAGAAHYWMBWYBKCMATYKAYKAGAGSNNNNN 643
1138 AAAATGATGACGAAAAAGAGTACAGATCCCATGCAAAATCTTGTCTTCTCAG 1197
644 NNNNNNNNNNATGARDVYAAASRYAMAAKMYYYKBAANNAVYTHANNMWGCMNATD 703
1198 CGTACTTACCACAAAATAGACTCTGAATAGGCCA 1233
704 TRRTMKNNNNNNAGTWKNNNNNAKNVAA 739
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RESULT 7
US-09-806-708B-22/c
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806, 708B
PRIORITY FILING DATE: 2001-04-03
PRIORITY FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA

ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Promoter
LOCATION: (1..1141)
OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 3.4%, Score 43.6; DB 4; Length 1141;
Best Local Similarity 13.2%; Pred. No. 0.0027; Indels 5; Gaps 1;
Matches 77; Conservative 192; Mismatches 309;

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690 TCTGATGAGAAACAGCTCTTCAAGTTTTCAGTGCATCATGTGTCAGATTCGCA 749
1100 TKSATGTAMWTHNAKAGATCMWYWTGTRRCKMRTYMTYTSNANWSCATGBMW 1041
750 GTCAAAATTTGATGTTTCTTTTACCATATCTTACCAAGCCGACAGAAATCAGCTG 809
1040 WTMKRYATKYRTAYAWMCAWRNNNNMCATNGYAKSCATNNAMVYATTBAAVYAAAKWAR 981
810 AAGCAATTTACCGAAGTTGTCAGAGAGTGTCTCAACATGCTTTGTGCACAGAT 869
980 WAGNNMMYGAAGNKKGCMAAMATWGBWADTAGKVCNNNNNNWTTDVERMAKAKNN 921
870 TTAAGAATCTTGTGATTTTCAAGATGATTAATGATGAGAAAGACTGTTGAT 929
920 NNNAYWTACYNRAATNNKATHTMMKTHGAHSKRTTHRTCRKTYNNNNNNARTVW 861
930 CTTAACAAAGAAAGCTGCTGATGATTTGAAAATGAATCTTAGAGCTGCTAGTAA 989
860 YHHAARBMWMAWTRTNNNNNNNNNACRMTFTWABMKSHSCNNNNNNNNNNNTWC 801
990 GTGTGAGAAATGTAAGAGCTCAGACCAAGTTAAATCCCTTTCTCAGAAATCCT 1049
800 HYTANABBCYRANNNNAARMAFTCNVYHAAATTTHTWCKYTWNTWYDMTMTBT 741
1050 GATGAATTTATGATCCAAATAGTAGAGAACTTATGAAGATCCGCTATGCTCAGAT 1109
740 TTRNNMTTSTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 686
1110 GCGTATTCATATGAGAAAGAGCAATGAGAAATTTGATCAGCAAAAGAAAGTAC 1169
685 NNTVMRRMMWNTNKTMYSTTRRHHTGATNNNNNNNNNNNNNNNNNNNNNNNNNN 626
1170 CCCATGCAAAATCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1229
625 TMDGDTVRKVAWRTCTTYVDVWADSWWVYANMRCRDVYTRNNYCKSYASHYW 566
1230 GCCATCAATAGATGCTGAGACACACCAAGTAAAGAAATTC 1272
565 YMSNNAMWYRRYSARRNSSMARWTRNNNNWMSGBVRWRWAGTM 523
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RESULT 8
US-10-101-464A-251
Sequence 251, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101, 464A
PRIORITY FILING DATE: 2002-03-18
PRIORITY FILING DATE: 2000-11-01
PRIORITY FILING DATE: 09/704, 302
PRIORITY FILING DATE: 09/228, 986
PRIORITY FILING DATE: 1999-01-12
PRIORITY FILING DATE: 60/162, 866
PRIORITY FILING DATE: 1999-11-01
PRIORITY FILING DATE: PCT/US00/00724
PRIORITY FILING DATE: 2000-01-11

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/ NUMBER OF SEQ ID NOS: 989
/ SOFTWARE: ParseSeq for Windows Version 4.0
/ SEQ ID NO 251
/ LENGTH: 937
/ TYPE: DNA
/ ORGANISM: Eucalyptus grandis
US-10-101-464A-251

Query Match      3.4% Score 43; DB 4; Length 937;
Best Local Similarity 51.9%; Pred. No. 0.0037;
Matches 97; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1060 TATGTCCTTCTAGAGAACTTATGAAGATCCGGTATCGATCGATGCGCTATTCAT 1119
    |||||
DB 732 TGTGCCCATCTTTCAGGAATATATGATGATCTCTGATTTGGCGGATGTTTCACTT 791
    |||||
QY 1120 ATGAAGAAGACGACATGGAATAATTGATCAGCAAAAAGAAAGTCCATGACAA 1179
    |||||
DB 792 ATGAAGAGAGAGCTATCGGGAATGTTGACAAACGACGATACATCCGCAATGACCA 851
    |||||
QY 1180 ATCTTGTCTTCTCCTTCAGCGGTACTTACACCAATAGAGCTGGAATGGCCATCAATA 1239
    |||||
DB 852 ACTTGAAGCTTAGTATGATTTGATTCATCTCCTCAACGACGCTTACGGTGGCAATTCAG 911
    |||||
QY 1240 GATGGCT 1246
    |||||
DB 912 AGTGGCT 918

RESULT 9
US-09-345-882-1/c
/ Sequence 1, Application US/09345882
/ Patent No. 6393373
/ GENERAL INFORMATION:
/ APPLICANT: Bouquelerec, Lydie
/ TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
/ FILE REFERENCE: GENSET.031A
/ CURRENT APPLICATION NUMBER: US/09/345,882
/ CURRENT FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: US 60/091,315
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/111,909
/ PRIOR FILING DATE: 1998-12-10
/ NUMBER OF SEQ ID NOS: 140
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1
/ LENGTH: 162450
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 72794 : polymorphic base A or G
/ OTHER INFORMATION: 5-124-273 : polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 88073 : polymorphic base A or G
/ OTHER INFORMATION: 5-127-261 : polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 93714 : polymorphic base A or G
/ OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 97122 : polymorphic base G or T
/ OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 97152 : polymorphic base deletion of T

/ OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99098 : polymorphic base A or G
/ OTHER INFORMATION: 5-130-257 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 99117 : polymorphic base A or G
/ OTHER INFORMATION: 5-130-276 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 103806 : polymorphic base A or T
/ OTHER INFORMATION: 5-131-395 : polymorphic base A or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 106940 : polymorphic base insertion of A
/ OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108106 : polymorphic base insertion of A
/ OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108149 : polymorphic base insertion of GTTT
/ OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108308 : polymorphic base A or G
/ OTHER INFORMATION: 5-135-357 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 108471 : polymorphic base C or T
/ OTHER INFORMATION: 5-136-174 : polymorphic base C or T
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/ LOCATION: 134134 : polymorphic base C or T
/ OTHER INFORMATION: 5-140-120 : polymorphic base C or T
/ FEATURE:
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/ LOCATION: 134362 : polymorphic base insertion of A
/ OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
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/ LOCATION: 146328 : polymorphic base A or G
/ OTHER INFORMATION: 5-143-84 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 146345 : polymorphic base A or C
/ OTHER INFORMATION: 5-143-101 : polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 150329 : polymorphic base A or G
/ OTHER INFORMATION: 5-145-24 : polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 160031 : polymorphic base G or T
/ OTHER INFORMATION: 5-148-352 : polymorphic base G or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID30
/ OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID30
/ OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 88050..88096 : polymorphic fragment 5-127-261 SEQ ID31
/ OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match 3.1%; Score 40; DB 2; Length 246240;
Best Local Similarity 55.9%; Pred. No. 1.9;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 773 TACCATATCTTAGCAGAGCGCACAGAACATCAGTGAAGCAATTTACCGAAGATTGTC 832
DB 45039 TACTCATGCTGTGATGAATTTACCAAAACATACCCCTGGCCAAATTAACAAACAGCAGAGC 45098
QY 833 AAGAGAGCTGCTTCAACATGCTTTGTGACAAAGATTTAAAGATCTTGTGATTTT 892
DB 45099 AATGTGTTGTGTGTATMACTTTCTACCAAAATACGAAAAAAGTGAATTCATGTT 45158
QY 893 CAAGATGAATTAACATT 908
DB 45159 CAGCATTAATTAATTT 45174

RESULT 13
US-08-724-394A-21
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

Query Match 3.1%; Score 40; DB 2; Length 246240;
Best Local Similarity 55.9%; Pred. No. 1.9;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 773 TACCATATCTTAGCAGAGCGCACAGAACATCAGTGAAGCAATTTACCGAAGATTGTC 832
DB 45039 TACTCATGCTGTGATGAATTTACCAAAACATACCCCTGGCCAAATTAACAAACAGCAGAGC 45098
QY 833 AAGAGAGCTGCTTCAACATGCTTTGTGACAAAGATTTAAAGATCTTGTGATTTT 892
DB 45099 AATGTGTTGTGTGTATMACTTTCTACCAAAATACGAAAAAAGTGAATTCATGTT 45158
QY 893 CAAGATGAATTAACATT 908
DB 45159 CAGCATTAATTAATTT 45174

RESULT 14
US-08-724-394A-22
Sequence 22, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereo
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match 3.1%; Score 40; DB 2; Length 246240;
Best Local Similarity 55.9%; Pred. No. 1.9;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 773 TACCCATATCTTAGCAAGGCGCACAGAACATCAGCTGAGCAATTTACCGAGATTGTC 832
DB 45039 TACTCATGCTGTGATGAAGTATTACCAACATACCCCTGGGCCAATTAACMAAGCAGAGC 45098
QY 833 AGAGAGAGTGTCTCAACATGCTTGTGCAAGAATTTAAAGATCTTGTGTAATTT 892
DB 45099 AATGTGTTGTGTGTGTATTAATTTCTACACAAATACAGAAAAGTGAATTCATTT 45158
QY 893 CAAGATGAATTAACATT 908
DB 45159 CAGCATAAATAAATTT 45174

RESULT 15
US-09-690-364-10
; Sequence 10, Application US/09690364
; Patent No. 6468795
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF APAF-1 EXPRESSION
; FILE REFERENCE: RTS-0190
; CURRENT APPLICATION NUMBER: US/09/690,364
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 10
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (586)...(4302)
US-09-690-364-10

Query Match 3.1%; Score 39.6; DB 3; Length 5152;
Best Local Similarity 54.9%; Pred. No. 0.16;
Matches 78; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 442 GTTTGGCATCAGGGGAGCTGATGAACCTGTGTTTGTGAATGCACAGTCATACAAAT 501
DB 3722 GATTGCTTCTTGTCATTGATGAACGGTGAAGGTGAGATGCATTACCGAAGAA 3781
QY 502 TATATGATGTGTAGTAAAGATGCTCTTGCGGCGATGTCATTTCTCTAATG 561
DB 3782 TAGAAGAGACTTTACTTGTGCATCAGGGGACAGTGCTTCTGTGTATCTCTTGATG 3841
QY 562 GAAGCTTCTTGTCACTGGCTC 583
DB 3842 CGACCAAGTTTCTCTACCTC 3863

Search completed: October 25, 2005, 07:46:32
Job time : 185 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 06:52:11 : Search time 2669 Seconds
(without alignments)
3933.065 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272

Sequence: 1 gaattcggttcctaccctgcg.....acaccaaagttaagaattc 1272

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9772377 seqs, 4126317084 residues

Total number of hits satisfying chosen parameters: 19544754

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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20: /cgn2_6/prodata/2/pubpna/US10G_PUBCOMB.seq:*
21: /cgn2_6/prodata/2/pubpna/US10H_PUBCOMB.seq:*
22: /cgn2_6/prodata/2/pubpna/US10I_PUBCOMB.seq:*
23: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
24: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq2:*
25: /cgn2_6/prodata/2/pubpna/US11_PUBCOMB.seq:*
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28: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1272	100.0	1272	14	US-10-077-111-12 Sequence 12, Appl
2	977.2	76.8	1553	14	US-10-077-111-3 Sequence 3, Appl
3	965.8	75.9	1818	14	US-10-077-111-1 Sequence 1, Appl
4	964.2	75.8	1817	10	US-09-971-392-207 Sequence 207, App
5	964.2	75.8	1821	22	US-10-956-157-5128 Sequence 5128, Ap

6	964.2	75.8	1844	16	US-10-037-270-768 Sequence 768, App
7	964.2	75.8	1844	18	US-10-117-722-768 Sequence 768, App
8	894	70.3	1773	17	US-10-287-218-40 Sequence 40, Appl
9	894	70.3	1773	20	US-10-474-291-40 Sequence 40, Appl
10	890.2	70.0	1811	18	US-10-104-047-1689 Sequence 1689, Ap
11	878.8	69.1	1996	21	US-10-357-930-23179 Sequence 23179, A
12	878.8	69.1	1996	21	US-10-357-930-29046 Sequence 29046, A
13	877.8	69.0	1908	14	US-10-077-111-14 Sequence 14, Appl
14	602.2	47.3	1400	22	US-10-956-157-1063 Sequence 1063, A
15	464	36.5	1901	14	US-10-077-111-6 Sequence 6, Appl
16	377.2	29.7	630	14	US-10-077-111-5 Sequence 5, Appl
17	335	26.3	446	21	US-10-357-930-5029 Sequence 5029, Ap
18	331.6	26.1	366	9	US-09-864-761-10657 Sequence 10657, Ap
19	329.8	25.9	409	21	US-10-357-930-14198 Sequence 14198, A
20	328.8	25.8	441	21	US-10-357-930-35319 Sequence 35319, A
21	328.8	25.8	441	21	US-10-357-930-44154 Sequence 44154, A
22	297	23.3	297	9	US-09-864-761-27306 Sequence 27306, A
23	291.6	22.9	419	24	US-10-779-543-8962 Sequence 8962, Ap
24	179.6	14.1	466	9	US-09-864-761-11052 Sequence 11052, A
25	176.8	13.9	180	9	US-09-864-761-27687 Sequence 27687, A
26	154	12.1	520	14	US-10-077-111-8 Sequence 8, Appl
27	146.6	11.5	399	24	US-10-779-543-12137 Sequence 12137, A
28	142.6	11.2	480	9	US-09-864-761-13978 Sequence 13978, A
29	132	10.4	132	9	US-09-864-761-30542 Sequence 30542, A
30	129.4	10.2	604	13	US-09-925-065A-667748 Sequence 667748, A
31	129.4	10.2	604	13	US-09-925-065A-667749 Sequence 667749, A
32	129.4	10.2	604	13	US-09-925-065A-667750 Sequence 667750, A
33	129.4	10.2	604	13	US-09-925-065A-667751 Sequence 667751, A
34	129.4	10.2	604	13	US-09-925-065A-667752 Sequence 667752, A
35	118.2	9.3	478	10	US-09-918-995-13423 Sequence 13423, A
36	92	7.2	428	14	US-10-027-632-62257 Sequence 62257, A
37	92	7.2	428	14	US-10-027-632-62257 Sequence 62257, A
38	91	7.2	428	14	US-10-027-632-35838 Sequence 35838, A
39	91	7.2	428	14	US-10-027-632-35838 Sequence 35838, A
40	87	6.8	92	16	US-10-106-698-3381 Sequence 3381, Ap
41	76	6.0	439	14	US-10-027-632-195937 Sequence 195937, A
42	76	6.0	439	18	US-10-027-632-195937 Sequence 195937, A
43	70	5.5	573	13	US-09-925-065A-736064 Sequence 736064, A
44	62.8	4.9	2511	18	US-10-260-238-549 Sequence 549, App
45	62.8	4.9	2813	20	US-10-437-963-64112 Sequence 64112, A

ALIGNMENTS

RESULT 1
US-10-077-111-12
Sequence 12, Application US/10077111
Publication No. US20020187492A1
GENERAL INFORMATION:
APPLICANT: Toddard, C. Gordon
APPLICANT: Finger, Joshua N.
APPLICANT: Rillema, Jill
TITLE OF INVENTION: TBA
FILE REFERENCE: 3053-4114US2
CURRENT APPLICATION NUMBER: US/10/077, 111
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/294,181
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/269,366
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1272
TYPE: DNA
ORGANISM: HUMAN
FEATURES:
OTHER INFORMATION: RET 16.2 splice variant
US-10-077-111-12
Query Match 100.0%; Score 1272; DB 14; length 1272;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCTTTACCGTGGCGGCGAGGTGACCGCGACCGCGCGTGGGACCTTTGAAGGGG 60
DB 1 GAATTCGGCTTTACCGTGGCGGCGAGGTGACCGCGACCGCGCGTGGGACCTTTGAAGGGG 60
QY 61 GATCCCGCGCGCGCGCGCTCTGCAAGCTGTCTTTCTTCAATTAAGAACATGGTGAAC 120
DB 61 GATCCCGCGCGCGCGCGCTCTGCAAGCTGTCTTTCTTCAATTAAGAACATGGTGAAC 120
QY 121 TGATTACACATTAAGTGCATAGTGAGCATGTCAACTGCTGTCTTCTCTTTCC 180
DB 121 TGATTACACATTAAGTGCATAGTGAGCATGTCAACTGCTGTCTTCTCTTTCC 180
QY 181 TCTTGCTACTTGTCTCTTGGACAAACAAATTCGCTGTACTGTGTTACGATCTTACTG 240
DB 181 TCTTGCTACTTGTCTCTTGGACAAACAAATTCGCTGTACTGTGTTACGATCTTACTG 240
QY 241 AACTGCGACATTTCTCAATGTAAGTTTCAATCCTATGCTGTCACTGCTGCTTTCTCC 300
DB 241 AACTGCGACATTTCTCAATGTAAGTTTCAATCCTATGCTGTGTCACTGCTGCTTTCTCC 300
QY 301 CTTCAGAGACATATTTTGGCATCTGTCTTCAACAGATGTACACTGTCTTATGGAATCTG 360
DB 301 CTTCAGAGACATATTTTGGCATCTGTCTTCAACAGATGTACACTGTCTTATGGAATCTG 360
QY 361 AAAATGACAGATGTGCGAGTATGGAACAGCCTAGTGCGACCGCTGTAGGGGTTTCC 420
DB 361 AAAATGACAGATGTGCGAGTATGGAACAGCCTAGTGCGACCGCTGTAGGGGTTTCC 420
QY 421 AGTTTTCGCCAGCTCCACGCTGTTTGGCATCAGGGGACGCTGATGGAATCTGTGTTTGT 480
DB 421 AGTTTTCGCCAGCTCCACGCTGTTTGGCATCAGGGGACGCTGATGGAATCTGTGTTTGT 480
QY 481 GGAATGACAGATGTGCGAGTATGGAACAGCCTAGTGCGACCGCTGTAGGGGTTTCC 540
DB 481 GGAATGACAGATGTGCGAGTATGGAACAGCCTAGTGCGACCGCTGTAGGGGTTTCC 540
QY 541 CATGTGCATTTTCTCTTAATGTAAGCTTCTTGTCTCACTGCTCTCATGTGTGATTTAA 600
DB 541 CATGTGCATTTTCTCTTAATGTAAGCTTCTTGTCTCACTGCTCTCATGTGTGATTTAA 600
QY 601 CAGTGTGGAGTATTAAGTGTGTCTGTGATAGTGAAGAACATGATCTTGAATTA 660
DB 601 CAGTGTGGAGTATTAAGTGTGTCTGTGATAGTGAAGAACATGATCTTGAATTA 660
QY 661 CCGTGTGGCATTTTCTCTTCAAGCAGCTTCTTGTCTCACTGCTCTCATGTGTGATTTAA 720
DB 661 CCGTGTGGCATTTTCTCTTCAAGCAGCTTCTTGTCTCACTGCTCTCATGTGTGATTTAA 720
QY 721 GACTGGCATCATGTGTGATGAGATTTGCCAAGTCAAAATTTGATTTGTTCTTTAACCATA 780
DB 721 GACTGGCATCATGTGTGATGAGATTTGCCAAGTCAAAATTTGATTTGTTCTTTAACCATA 780
QY 781 TCTTACGAAGGCGCACAGAACATCAGCTGAAGCAATTTACGAAATTTGGTTCAGAGAGG 840
DB 781 TCTTACGAAGGCGCACAGAACATCAGCTGAAGCAATTTACGAAATTTGGTTCAGAGAGG 840
QY 841 TCGTCTCAACATGGCTTTGTGCAAGATTTAAAGATCTTGTGTGATTTTCAAGATGA 900
DB 841 TCGTCTCAACATGGCTTTGTGCAAGATTTAAAGATCTTGTGTGATTTTCAAGATGA 900
QY 901 ATTAACATTGATGAAAAAGAACTGTGATCTTCAAAAGAAAGTGTGCTGATGATTTGA 960
DB 901 ATTAACATTGATGAAAAAGAACTGTGATCTTCAAAAGAAAGTGTGCTGATGATTTGA 960
QY 961 AAATTGAATCTCTAGAGCTGCGTAGTAAGTGTGAGAAATTTGAAAGCTCAGAGCA 1020
DB 961 AAATTGAATCTCTAGAGCTGCGTAGTAAGTGTGAGAAATTTGAAAGCTCAGAGCA 1020
QY 1021 AGGTTAAATCCCTTTCTTCAAGAAATTCGATGAATTTATATGTCATTAATCTAGAGAAC 1080
DB 1021 AGGTTAAATCCCTTTCTTCAAGAAATTCGATGAATTTATATGTCATTAATCTAGAGAAC 1080

QY 1081 TTATGAAGATCCGTCATCGCATGATGCTGATTTATATGAAAAAGAACATGGA 1140
DB 1081 TTATGAAGATCCGTCATCGCATGATGCTGATTTATATGAAAAAGAACATGGA 1140
QY 1141 ATTGATCAGCAAAAGAAAGCTACAGTCCCATGACAAATCTTCTTCTTACGGG 1200
DB 1141 ATTGATCAGCAAAAGAAAGCTACAGTCCCATGACAAATCTTCTTCTTACGGG 1200
QY 1201 TACTTACCAAAATGAGCTCTGAAATGCGCATCAATGATGCTGAGACACCA 1260
DB 1201 TACTTACCAAAATGAGCTCTGAAATGCGCATCAATGATGCTGAGACACCA 1260
QY 1261 AGTAAGAATTC 1272
DB 1261 AGTAAGAATTC 1272

RESULT 2
US-10-077-111-3
; Sequence 3, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Toddard, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: HUMAN
US-10-077-111-3

Query Match 76.8%; Score 977.2; DB 14; Length 1553;
Best Local Similarity 81.9%; Pred. No. 3,8e-274;
Matches 1265; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 1 GAATTCGGCTTTACCGTGGCGGCGAGGTGACCGCGACCGCGCGTGGGACCTTTGAAGGGG 60
DB 1 GAATTCGGCTTTACCGTGGCGGCGAGGTGACCGCGACCGCGCGTGGGACCTTTGAAGGGG 60
QY 61 GATCCCGCGCGCGCGCGCTCTGCAAGCTGTCTTTCTTCAATTAAGAACATGGTGAAC 120
DB 61 GATCCCGCGCGCGCGCGCTCTGCAAGCTGTCTTTCTTCAATTAAGAACATGGTGAAC 120
QY 121 TGATTACACATTAAGTGCATAGTGAGCATGTCAACTGCTGTCTTCTCTTTCC 180
DB 121 TGATTACACATTAAGTGCATAGTGAGCATGTCAACTGCTGTCTTCTCTTTCC 180
QY 181 TCTTGCTACTTGTCTCTTGGACAAACAAATTCGCTGTACTGTGTTACGATCTTACTG 240
DB 181 TCTTGCTACTTGTCTCTTGGACAAACAAATTCGCTGTACTGTGTTACGATCTTACTG 240
QY 241 AACTGCGACATTTCTCAATGTAAGTTTCAATCCTATGCTGTGTCACTGCTGCTTTCTCC 300
DB 241 AACTGCGACATTTCTCAATGTAAGTTTCAATCCTATGCTGTGTCACTGCTGCTTTCTCC 300
QY 301 CTTCAGAGACATATTTTGGCATCTGTCTTCAACAGATGTACACTGTCTTATGGAATCTG 360
DB 301 CTTCAGAGACATATTTTGGCATCTGTCTTCAACAGATGTACACTGTCTTATGGAATCTG 360
QY 361 AAAATGACAGATGTGCGAGTATGGAACAGCCTAGTGCGACCGCTGTAGGGGTTTCC 420
DB 361 AAAATGACAGATGTGCGAGTATGGAACAGCCTAGTGCGACCGCTGTAGGGGTTTCC 420


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QY 612 GATMAAATGAGTGTCTGCTAGTAGTGAAGAACATGATCTTGGAAATTACCTGCGCAT 671
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Db 649 GATMAAATGAGTGTCTGCTAGTAGTGAAGAACATGATCTTGGAAATTACCTGCGCAT 708
| | | | |
QY 672 TTTTCTTACAGCCAGCTTTCTGATGGAACAAAGCTTTTCAAGTTTTTGCATGCGCATCA 731
| | | | |
Db 709 TTTTCTTACAGCCAGCTTTCTGATGGAACAAAGCTTTTCAAGTTTTTGCATGCGCATCA 768
| | | | |
QY 732 TGTGCTCAGAGTGGCCAAAGTCAAAATTTGGATTGTTCTTTTACCCCATCTT----- 784
| | | | |
Db 769 TGTGCTCAGAGTGGCCAAAGTCAAAATTTGGATTGTTCTTTTACCCCATCTTAGGTTT 828
| | | | |
QY 785 ----- 784
| | | | |
Db 829 GAATTAATAATATAAGTACACTGAGTGGGCACTGTGCTCTGTTTGGCTTGGCTTTT 888
| | | | |
QY 785 ----- 784
| | | | |
Db 889 TCCCATGATGGGAGATGCTAGTCTCAGGGTCAGTGGATTAAGTCTGTCAATAGTATAGAT 948
| | | | |
QY 785 ----- 784
| | | | |
Db 949 ACTAATACTGAGAAATATCTTCAACATTTGACTCAGACACCAAGTATGTCAACAATTGT 1008
| | | | |
QY 785 ----- 784
| | | | |
Db 1009 GCTTTTGCACTAATACCTTTTACTTGTCTAGTGTTCATATGACAAACAGTGAACATC 1068
| | | | |
QY 785 -----AGCAAGGGGCGACAGAACTCAAGCTGGAAGCA 815
| | | | |
Db 1069 TGGCAATTTGACCTGGAAACATTTTGGCAAGCAAGGGGCAAGAACTCAAGCTGGAAGCA 1128
| | | | |
QY 816 TTTTACCGAATTTGATGTCAGAGAGTGTCTCAACATGCTGTTGTGCAAGATTTTAA 875
| | | | |
Db 1129 TTTTACCGAATTTGATGTCAGAGAGTGTCTCAACATGCTGTTGTGCAAGATTTTAA 1188
| | | | |
QY 876 GATCTTGTGGTATTTTCAAGATGAATTAACATTGATGAAAGAACTGTTGAATCTTTACA 935
| | | | |
Db 1189 GATCTTGTGGTATTTTCAAGATGAATTAACATTGATGAAAGAACTGTTGAATCTTTACA 1248
| | | | |
QY 936 AAGAAGAGTGTGCTGATGATTTTGAAGATTTGAACTCTTGAAGATCTGCTATGAAGTCTG 995
| | | | |
Db 1249 AAGAAGAGTGTGCTGATGATTTTGAAGATTTGAACTCTTGAAGATCTGCTATGAAGTCTG 1308
| | | | |
QY 996 AGAAATTTGAAGAGTCTCAGACCAAGGTTAAATCCCTTTCTTCAAGAAATTCCTGATGAA 1055
| | | | |
Db 1309 AGAAATTTGAAGAGTCTCAGACCAAGGTTAAATCCCTTTCTTCAAGAAATTCCTGATGAA 1368
| | | | |
QY 1056 TTTATATGTCCTAATTAAGAGAACTTATGAAAGATCCGGTCAATCCGATCAGATGGCTAT 1115
| | | | |
Db 1369 TTTATATGTCCTAATTAAGAGAACTTATGAAAGATCCGGTCAATCCGATCAGATGGCTAT 1428
| | | | |
QY 1116 TCTATATGAAGAGAGCAATGCAAAATTTGATCAGCAAAAGAAAGCTTACAACTGCCATG 1175
| | | | |
Db 1429 TCTATATGAAGAGAGCAATGCAAAATTTGATCAGCAAAAGAAAGCTTACAACTGCCATG 1488
| | | | |
QY 1176 ACAAAATCTTGTCTTCTTCTCAGCGGTACTTACACCAAAATAGACTCTGAAGATGGCCATC 1235
| | | | |
Db 1489 ACAAAATCTTGTCTTCTTCTCAGCGGTACTTACACCAAAATAGACTCTGAAGATGGCCATC 1548
| | | | |
QY 1236 AATAGATGGCTGAGACACACCAAAAGTAA 1266
| | | | |
Db 1549 AATAGATGGCTGAGACACACCAAAAGTAA 1579
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RESULT 4
US-09-971-392-207
; Sequence 207, Application US/09971392

; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Cocke, Benjamin G.

```
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0029 US  
; CURRENT APPLICATION NUMBER: US/09/971,392  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/237,652  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 260  
; SOFTWARE: PERL Program  
; SEQ ID NO 207  
; LENGTH: 1817  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Template ID: 158923.9  
US-09-971-392-207
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Query Match 75.8%; Score 964.2; DB 10; Length 1817;
Best Local Similarity 81.8%; Pred. No. 2,78-270;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

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QY 12 TCACCTGGCGGCGACGTCGACCCGACCCGCTGGGACCTTGAAGCGCGATCCCGCGG 71
| | | | |
Db 49 TCACCTGGCGGCGACGTCGACCCGACCCGCTGGGACCTTGAAGCGCGATCCCGCGG 108
| | | | |
QY 72 CCCCCGCTCCTGAGGCTGTTTTTCTTCAATTAAGAACTGGAATTCACACA 131
| | | | |
Db 109 CCCCCGCTCCTGAGGCTGTTTTTCTTCAATTAAGAACTGGAATTCACACA 168
| | | | |
QY 132 TTAGCTGATCATGCTGACATGTCATGCTGCTTCTCTTCTTCTTCTTCTTCTTCTTCT 191
| | | | |
Db 169 TTAGCTGATCATGCTGACATGTCATGCTGCTTCTCTTCTTCTTCTTCTTCTTCTTCT 228
| | | | |
QY 192 TGTCTCTTGAGCAAAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
| | | | |
Db 229 TGTCTCTTGAGCAAAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
| | | | |
QY 252 TCTCATTGAAGTTGATACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
| | | | |
Db 289 TCTCATTGAAGTTGATACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
| | | | |
QY 312 ATTTTGGCATGCTGTTCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
| | | | |
Db 349 ATTTTGGCATGCTGTTCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
| | | | |
QY 372 ATGCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
| | | | |
Db 409 ATGCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
| | | | |
QY 432 GACTCAGCTGTTTGGCATCAGGGGAGCTGATGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
| | | | |
Db 469 GACTCAGCTGTTTGGCATCAGGGGAGCTGATGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
| | | | |
QY 492 TCTATCAAAATTAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
| | | | |
Db 529 TCTATCAAAATTAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
| | | | |
QY 552 TCTCCTTAATGGAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
| | | | |
Db 589 TCTCCTTAATGGAAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
| | | | |
QY 612 GATMAAATGAGTGTCTGCTAGTAGTGAAGAACATGATCTTGAATTAACCTGCTGCGAT 671
| | | | |
Db 649 GATMAAATGAGTGTCTGCTAGTAGTGAAGAACATGATCTTGAATTAACCTGCTGCGAT 708
| | | | |
QY 672 TTTTCTTACAGCCAGCTTTCTGATGGAACAAAGCTTTTCAAGTTTTTGCATGCGCATCA 731
| | | | |
Db 709 TTTTCTTACAGCCAGCTTTCTGATGGAACAAAGCTTTTCAAGTTTTTGCATGCGCATCA 768
| | | | |
QY 732 TGTGCTCAGAGTGGCCAAAGTCAAAATTTGGATTGTTCTTTTACCCCATCTT----- 784
| | | | |
Db 769 TGTGCTCAGAGTGGCCAAAGTCAAAATTTGGATTGTTCTTTTACCCCATCTTAGGTTT 828
| | | | |
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QY 785 ----- 784
Db 829 GAATTAATAATAAGTACACTGAGTGGGCACTGCTCTCTGTTCTGGCTTGCTTT 888
QY 785 ----- 784
Db 889 TCCCATGATGGGAGATGCTAGTCTCAGGGTCAATGATAGTCTGTCATATATATGAT 948
QY 785 ----- 784
Db 949 ACTAATACTGAGAAATATACTTCAACATTGACTCAGACACAGATATGTCACAACCTGT 1008
QY 785 ----- 784
Db 1009 GCTTTTGACCTAATAACCTTTTACTTGCTAGTCTGTTCAATGACAAACAGTACATC 1068
QY 785 ----- -AGCAAGGCGCACAGAACATCAGCTGAGCA 815
Db 1069 TGGCAATTGACCTGGAACACTTTGGCAAGCAAGACAGAACATCAGCTGAGCA 1128
QY 816 TTTACCGAAGATGCTGAGAGAGTGTCTCAACATGGCTTTGTGACAAAGATTTTAAA 875
Db 1129 TTTACCGAAGATGCTGAGAGAGTGTCTCAACATGGCTTTGTGACAAAGATTTTAAA 1188
QY 876 GATCTTGTGATATTTCAAGATGATATACATGATGAAAAAGAACTGTTGAATCTTACA 935
Db 1189 GATCTTGTGATATTTCAAGATGATATACATGATGAAAAAGAACTGTTGAATCTTACA 1248
QY 936 AAAAGAAAGTGTGCTGATGATTTGAAAAATTGAATCTGAGACTGCTGATGAAAGTCTG 995
Db 1249 AAAAGAAAGTGTGCTGATGATTTGAAAAATTGAATCTGAGACTGCTGATGAAAGTCTG 1308
QY 996 AGCAAAATTTGAAGAGCTCAGAGCAACCAAGTTAAATCCCTTTCTTGAAGAAATTCCTGATGAA 1055
Db 1309 AGCAAAATTTGAAGAGCTCAGAGCAACCAAGTTAAATCCCTTTCTTGAAGAAATTCCTGATGAA 1368
QY 1056 TTTATATGCTCAATATATAGAGAACTTATGAAAGATCCGGTCAATGATGATGATGATGAT 1115
Db 1369 TTTATATGCTCAATATATAGAGAACTTATGAAAGATCCGGTCAATGATGATGATGATGAT 1428
QY 1116 TCATATGAAAAAGAAAGCAATGAAAAATTGATCAGCAAAAAAGAAACGTACAAATGCCATG 1175
Db 1429 TCATATGAAAAAGAAAGCAATGAAAAATTGATCAGCAAAAAAGAAACGTACAAATGCCATG 1488
QY 1176 ACAAAATCTTGTCTCTCTTCAAGCGGTACTTACACCAAAATAGAGATCTGAAAAATGCCATC 1235
Db 1489 ACAAAATCTTGTCTCTCTTCAAGCGGTACTTACACCAAAATAGAGATCTGAAAAATGCCATC 1548
QY 1236 AATAGATGGCTGAGACACACCAAAAGTAAA 1266
Db 1549 AATAGATGGCTGAGACACACCAAAAGTAAA 1579

RESULT 5
US-10-956-157-5128 : Sequence 5128, Application US/10956157
: Publication No. US20050118625A1
: GENERAL INFORMATION:
: APPLICANT: Wyeth
: APPLICANT: Mounts, William
: TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
: FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
: FILE REFERENCE: 031896-043000 (AM 101081)
: CURRENT APPLICATION NUMBER: US/10/956,157
: NUMBER OF SEQ ID NOS: 319805
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 5128
: LENGTH: 1821
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-956-157-5128
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Query Match 75.8%; Score 964.2; DB 22; Length 1821;
Best Local Similarity 81.8%; Pred. No. 2,7e-270;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 12 TCACCTGCGGAGCAGTGACCGGACCGCCGTTGGGACCTTGAAGGGATCCCGCG 71
Db 60 TCACCTGCGGAGCAGTGACCGGACCGCCGTTGGGACCTTGAAGGGATCCCGCG 119
QY 72 CCCCCGCTCTGAGAGCTGTTTTTTTCAATAAAGAACTGTTGAACATGATTCACACA 131
Db 120 CCCCCGCTCTGAGAGCTGTTTTTTTCAATAAAGAACTGTTGAACATGATTCACACA 179
QY 132 TTAGCTGATCATGATGACAGATGTCACATGCTGAGCTTCTCTCTTCCCTTGGACTACT 191
Db 180 TTAGCTGATCATGATGACAGATGTCACATGCTGAGCTTCTCTCTTCCCTTGGACTACT 239
QY 192 TGCTCTTGGACAAACCAATTTGCTGACTGTTACGATGACTTTACTGAATGCCACAT 251
Db 240 TGCTCTTGGACAAACCAATTTGCTGACTGTTACGATGACTTTACTGAATGCCACAT 299
QY 252 TCTCCATGAAAGTTTCAATACCTATGCTGCTGCTGCTGCTTCCGCCCTGAGACAT 311
Db 300 TCTCCATGAAAGTTTCAATACCTATGCTGCTGCTGCTGCTTCCGCCCTGAGACAT 359
QY 312 ATTTTGGACATGATGTTCAACAGATGTTACCACTGCTCTATGATAACTGAAAAATGACAG 371
Db 360 ATTTTGGACATGATGTTCAACAGATGTTACCACTGCTCTATGATAACTGAAAAATGACAG 419
QY 372 ATGCTGACATGATGAAACAGCTAGTGAGGAGCTGAGAGGCTTTGCGAGTTTTCGCCA 431
Db 420 ATGCTGACATGATGAAACAGCTAGTGAGGAGCTGAGAGGCTTTGCGAGTTTTCGCCA 479
QY 432 GACTCCACGTTGTTGGCATCAGGGGACGACTGATGAAACTGTGTTTGTGAAATGACAG 491
Db 480 GACTCCACGTTGTTGGCATCAGGGGACGACTGATGAAACTGTGTTTGTGAAATGACAG 539
QY 492 TCATACAAATTTATATAGATGTTGATGTTAAAGATGCTCTTGGCGGATGTCATTT 551
Db 540 TCATACAAATTTATATAGATGTTGATGTTAAAGATGCTCTTGGCGGATGTCATTT 599
QY 552 TCTCTTAATGAAAGCTTCTTGTCTACTGCTCTCATGTGTGATTTTAAACAGTGTGGAT 611
Db 600 TCTCTTAATGAAAGCTTCTTGTCTACTGCTCTCATGTGTGATTTTAAACAGTGTGGAT 659
QY 612 GATTAATAAGAGTGTCTGCTAGTGAAGAAAGACATCATCTTGTGAATTTACTCTGGAT 671
Db 660 GATTAATAAGAGTGTCTGCTAGTGAAGAAAGACATCATCTTGTGAATTTACTCTGGAT 719
QY 672 TTTTCTTCAAGCCAGTTTCTGATGAGAACAAAGTCTTCAATTTTTCGACTGGCATCA 731
Db 720 TTTTCTTCAAGCCAGTTTCTGATGAGAACAAAGTCTTCAATTTTTCGACTGGCATCA 779
QY 732 TGTGTCAGAGATTGCCAAGTCAAAATTTGATTTCTTTTAAACCAATCTT----- 784
Db 780 TGTGTCAGAGATTGCCAAGTCAAAATTTGATTTCTTTTAAACCAATCTTAAAGTTT 839
QY 785 ----- 784
Db 840 GAATTAATAATAAGTACACTGAGTGGGCACTGCTCTCTGCTTGTGCTTT 899
QY 785 ----- 784
Db 900 TCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGTAGTCTGTCATATATATGAT 959
QY 785 ----- 784
Db 960 ACTAATACTGAGAAATATACTTCAACATGATGACTCAGACACAGATATGTCACAATCTGT 1019
QY 785 ----- 784
Db 1020 GCTTTTGACCTAATAACCTTTTACTTGCTGATGCTTCAATGACAAACAGTGAACATC 1079
QY 785 ----- -AGCAAGGCGCACAGAACATCAGCTGAGCA 815
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Db 1080 TGGCAATTGACCTGGAAACATTGTCAGCAAGGGGCAAGAACATCGCTGAAAGCAA 1139
QY 816 TTTTACGGAAGATTGGTCAGAGAGGTCGTCTCAACATGGCTTTGTGCAAGATTTTAAA 875
Db 1140 TTTTACGGAAGATTGGTCAGAGAGGTCGTCTCAACATGGCTTTGTGCAAGATTTTAAA 1199
QY 876 GATCTTGTGGTATTTTCAAGATGAATACATTGATGGAAAAGAACTTGATCTTACA 935
Db 1200 GATCTTGTGGTATTTTCAAGATGAATACATTGATGGAAAAGAACTTGATCTTACA 1259
QY 936 AAGAAAGTCTGCTGATGATTTGAAAATTGAAATCTCTAGACCTGCTAGTAAAGTCTG 995
Db 1260 AAGAAAGTCTGCTGATGATTTGAAAATTGAAATCTCTAGACCTGCTAGTAAAGTCTG 1319
QY 996 AGGAAAATTGAAGAGCTCAGAGCAAGGTTAAATCCCTTTCTTCAGAAATTCCTGATGAA 1055
Db 1320 AGGAAAATTGAAGAGCTCAGAGCAAGGTTAAATCCCTTTCTTCAGAAATTCCTGATGAA 1379
QY 1056 TTTATATGTCCTAATTAAGATGAACTTAAGAAAGATCCGGTCATCGCATGAGATGGCTAT 1115
Db 1380 TTTATATGTCCTAATTAAGATGAACTTAAGAAAGATCCGGTCATCGCATGAGATGGCTAT 1439
QY 1116 TCATATGAAAAGAGCAATGAAAATTGGATGACAAAAGAAACGTACAAAGTCCCATG 1175
Db 1440 TCATATGAAAAGAGCAATGAAAATTGGATGACAAAAGAAACGTACAAAGTCCCATG 1499
QY 1176 ACAAAATCTGTTCTTCTCTTCCAGGGTACTTACACCAATAGACTCTGAAAATGGCCATC 1235
Db 1500 ACAAAATCTGTTCTTCTCTTCCAGGGTACTTACACCAATAGACTCTGAAAATGGCCATC 1559
QY 1236 AATAGATGGCTGGAGACACACCAAAAAGTAAA 1266
Db 1560 AATAGATGGCTGGAGACACACCAAAAAGTAAA 1590

RESULT 6

US-10-037-270-768
; Sequence 768, Application US/10037270
; Publication No. US20030104529A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungling
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhimei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,117
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pc_Fl_genes Version 1.0
SEQ ID NO 768
LENGTH: 1844
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-037-270-768

Query Match 75.8%; Score 964.2; DB 16; Length 1844;
Best Local Similarity 81.8%; Prod. No. 2.7e-270;
Matches 1252; Conservative 0; Mismatchen 3; Indels 276; Gaps 1;

QY 12 TCACCTGGCGGAGAGTGCACCCGACCCGCTGGGACCTTGAAGGCGGATCCCGCGG 71
Db 65 TCACCTGGCGGAGAGTGCACCCGACCCGCTGGGACCTTGAAGGCGGATCCCGCGG 124
QY 72 CCCCCGCTCTGCAAGCTGTTTTTTCTTCAATTAAGAACATGCTGAACATTCACACA 131
Db 125 CCCCCGCTCTGCAAGCTGTTTTTTCTTCAATTAAGAACATGCTGAACATTCACACA 184
QY 132 TTAGCTGATCATGTCAGATGTCATGCTGCTGCTTCTCTTTTCCCTTTGCTTACT 191
Db 185 TTAGCTGATCATGTCAGATGTCATGCTGCTGCTTCTCTTTTCCCTTTGCTTACT 244
QY 192 TGGTCTTGGACAAACATTTGGCTGTACTGTTACGTGACTTTACCTGACCTCCACAT 251
Db 245 TGGTCTTGGACAAACATTTGGCTGTACTGTTACGTGACTTTACCTGACCTCCACAT 304
QY 252 TCTCCATTGAAGTTTCTATACCTAAGCTGTCACCTGCTGCTTTTCCCTTCAGACAT 311
Db 305 TCTCCATTGAAGTTTCTATACCTAAGCTGTCACCTGCTGCTTTTCCCTTCAGACAT 364
QY 312 ATTTTGGCATCGTGTTCACACAGATGGTACACTGTCCTATGGAATACGAAAATGACAG 371
Db 365 ATTTTGGCATCGTGTTCACACAGATGGTACACTGTCCTATGGAATACGAAAATGACAG 424
QY 372 ATGCTGGCATGATGGAACAGCTTATGTCAGAGCCCTGTGAGGTTTGGCAATTTCCCA 431
Db 425 ATGCTGGCATGATGGAACAGCTTATGTCAGAGCCCTGTGAGGTTTGGCAATTTCCCA 484
QY 432 GACTCCAGTGTGTGGCATCAGGGGAGCTGATGGAACCTGTGTTTGTGAAATGACAG 491
Db 485 GACTCCAGTGTGTGGCATCAGGGGAGCTGATGGAACCTGTGTTTGTGAAATGACAG 544
QY 492 TCATCAAAATTATATAGATGTGTGATGTTAAAGATGCTCTTGGCGGATGTGATTT 551
Db 545 TCATCAAAATTATATAGATGTGTGATGTTAAAGATGCTCTTGGCGGATGTGATTT 604
QY 552 TCTCCCTAATGGAAGCTTTTGTGCACTGGCTCTCTCATGTGTGATTTAACAGTGTGGAT 611
Db 605 TCTCCCTAATGGAAGCTTTTGTGCACTGGCTCTCTCATGTGTGATTTAACAGTGTGGAT 664
QY 612 GATAAATGAGGTGCTGATAGTGAAGAACATGATCTTGAATTAACCTGTCGAT 671
Db 665 GATAAATGAGGTGCTGATAGTGAAGAACATGATCTTGAATTAACCTGTCGAT 724
QY 672 TTTTCTTCAACAGCAAGCTTTCTGATGGAACAAGTCTTCAAGTTTTCGATGCGATCA 731
Db 725 TTTTCTTCAACAGCAAGCTTTCTGATGGAACAAGTCTTCAAGTTTTCGATGCGATCA 784
QY 732 TGTGTGACAGATTGGCAAGTCAAAATTTGATTTGTTCTTTAACCAATCTT----- 784
Db 785 TGTGTGACAGATTGGCAAGTCAAAATTTGATTTGTTCTTTAACCAATCTT----- 844
QY 785 ----- 784
Db 845 GAATTAATAATTAAGTACACAGATGGGCACTGTGCTCTGCTTGTGCTTGT 904
QY 785 ----- 784
Db 905 TCCCATGATGGAGATGCTAGTCTCAGGGTCAATGATCTGTCAATGATATGAT 964
QY 785 ----- 784
Db 965 ACTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1024

QY 785 ----- 784
Db 1025 GCTTTGACCTAATACCCTTTTACTGTCTAGTGTTCATGACAAACAGTAACATC 1084
QY 785 ----- -AGCAAGCGCACAGAACATCAGCTGAACAA 815
Db 1085 TGGCAATTTGACCTGAAACCTTTGCCAAGCAAGACAGAACATCAGCTGAACAA 1144
QY 816 TTTACCGAAGATTTGTCAGAGAGAGTGTCTCAACATGCGCTTGTGACAAAGATTTAAA 875
Db 1145 TTTACCGAAGATTTGTCAGAGAGAGTGTCTCAACATGCGCTTGTGACAAAGATTTAAA 1204
QY 876 GATCTGTGTGTATTTTCAAGATGATACCTGATGAAAAGACTGTTGAATCTTACA 935
Db 1205 GATCTGTGTGTATTTTCAAGATGATACCTGATGAAAAGACTGTTGAATCTTACA 1264
QY 936 AAAAGAAAGTGTGCTGATGATTTGAAAATTTGAATCTCTAGAGACTGCGTAAAGTCTG 995
Db 1265 AAAAGAAAGTGTGCTGATGATTTGAAAATTTGAATCTCTAGAGACTGCGTAAAGTCTG 1324
QY 996 AGGAAATTTGAAGGCTCAGAGACCAAGTTAAATCCCTTTTTCAGGAATTCCTGATGAA 1055
Db 1325 AGGAAATTTGAAGGCTCAGAGACCAAGTTAAATCCCTTTTTCAGGAATTCCTGATGAA 1384
QY 1056 TTTATATGTCGAATTAATAGAACTTATGAAAAGATCCGGTCATCGCATCAGATGCGTAT 1115
Db 1385 TTTATATGTCGAATTAATAGAACTTATGAAAAGATCCGGTCATCGCATCAGATGCGTAT 1444
QY 1116 TCATATGAAAAAGAGCAATGGAATTTGATCGCAAAAAAGAAACGTACAGTCCCATG 1175
Db 1445 TCATATGAAAAAGAGCAATGGAATTTGATCGCAAAAAAGAAACGTACAGTCCCATG 1504
QY 1176 ACAAAATTTGTTCTCTCTTCAAGCGGTACTTAACACCAATAGAGACTCGAAAATGCCATC 1235
Db 1505 ACAAAATTTGTTCTCTCTTCAAGCGGTACTTAACACCAATAGAGACTCGAAAATGCCATC 1564
QY 1236 AATAGATGCGTCGAGACACACCAAAAGTAAA 1266
Db 1565 AATAGATGCGTCGAGACACACCAAAAGTAAA 1595

RESULT 7
US-10-117-722-768
; Sequence 768, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117, 722
; PRIORITY FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ. ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 768
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-117-722-768

Query Match 75.8%; Score 964.2; DB 18; Length 1844;
Best Local Similarity 81.8%; Pred. No. 2,7e-270;
Matches 1252; Conservative 0; Mismatches 3; Indels 276; Gaps 1;
QY 12 TCACCTGCGGAGACGTGACCCGACCGCCGTTGGACCTTGAAGCGGATCCCGCG 71
Db 65 TCACCTGCGGAGACGTGACCCGACCGCCGTTGGACCTTGAAGCGGATCCCGCG 124
QY 72 CCCCCGCTCTGACAGGTGTTTTTCTTCAATTAAGAACTGTTGAACATGATTCACACA 131
Db 125 CCCCCGCTCTGACAGGTGTTTTTCTTCAATTAAGAACTGTTGAACATGATTCACACA 184
QY 132 TTAGCTGATCATGATGACGATGTCACACTGCTGACCTTCCCTTTTCCCTTGGACTACT 191
Db 185 TTAGCTGATCATGATGACGATGTCACACTGCTGACCTTCCCTTTTCCCTTGGACTACT 244
QY 192 TGCTCTTTGACAAACAAATTCCTGTAAGTCTGTTAGCTGATTTACTGAATGCGACAT 251
Db 245 TGCTCTTTGACAAACAAATTCCTGTAAGTCTGTTAGCTGATTTACTGAATGCGACAT 304
QY 252 TCTCCATGAAAGTTTCTTACCTATGCTGTGCTGCTGCTGCTTTCCTCCCTTCAAGACAT 311
Db 305 TCTCCATGAAAGTTTCTTACCTATGCTGTGCTGCTGCTGCTTTCCTCCCTTCAAGACAT 364
QY 312 ATTTTGGCATGCTGTTCAACAGATGGTACCACTGCTCCTATGAAATAGACAG 371
Db 365 ATTTTGGCATGCTGTTCAACAGATGGTACCACTGCTCCTATGAAATAGACAG 424
QY 372 ATGCTGCACTGATGGAACAGCTTACGTGAGCGCTGTGAGGGTTTGCAGTTTTCGCCA 431
Db 425 ATGCTGCACTGATGGAACAGCTTACGTGAGCGCTGTGAGGGTTTGCAGTTTTCGCCA 484
QY 432 GACTCCACGTTTGGCATGAGGGGACGCTGATGGAACCTGCTGTTTGTGGAATGACAG 491
Db 485 GACTCCACGTTTGGCATGAGGGGACGCTGATGGAACCTGCTGTTTGTGGAATGACAG 544
QY 492 TCATACAAATTAATATGATGTGTAGTGTAAAGATGGCTCCTTGGCGCATGTCATTT 551
Db 545 TCATACAAATTAATATGATGTGTAGTGTAAAGATGGCTCCTTGGCGCATGTCATTT 604
QY 552 TCTCCTAATGAAAGCTTCTTGTCACTGCTCTCATGTGTGATTTAACAGTGTGGAT 611
Db 605 TCTCCTAATGAAAGCTTCTTGTCACTGCTCTCATGTGTGATTTAACAGTGTGGAT 664
QY 612 GATTAATAGAGTGTCTGCACTAGTAAAGACATGATCTTGGAAATTACTGCTGGAT 671
Db 665 GATTAATAGAGTGTCTGCACTAGTAAAGACATGATCTTGGAAATTACTGCTGGAT 724
QY 672 TTTTCTTCAAGCCAGTTTCTGATGGAACAAGGTCTTCAATTTTTCGACTGGCATCA 731
Db 725 TTTTCTTCAAGCCAGTTTCTGATGGAACAAGGTCTTCAATTTTTCGACTGGCATCA 784
QY 732 TGTGTCAGGATTTGCCAAGTCAAAATTTGGATGTTTCTTTTACCATATCTT----- 784
Db 785 TGTGTCAGGATTTGCCAAGTCAAAATTTGGATGTTTCTTTTACCATATCTTAAAGTTT 844
QY 785 ----- 784
Db 845 GAAATTAATATAAAGTACACTGATGAGGCACTGTGCTCTGTTCTGCTTGTGCTTTT 904
QY 785 ----- 784
Db 905 TCCCATGATGGCAGATGCTAGTCTCAGGCTCAGTGAATAAGTCTGTCATAGTATATGAT 964
QY 785 ----- 784
Db 965 ACTAATACGAGATATACTTCAACATGACTCAGACACCAAGTATGTCACAACTTGT 1024
QY 785 ----- 784
Db 1025 GCTTTTGCACCTAATACCCTTTTACTGTCTAGTGTTCATGACAAACAGTAACATC 1084
QY 785 ----- -AGCAAGCGCACAGAACATCAGCTGAACAA 815

Db 1085 TGGCAATTTGACCTGGAAACCTTTGGCAAGAGGACACAAATCAGTGGTGAAGCAA 1144
Qy 816 TTTTACGGAAGATTGCTCAGAGGAGTCTCTCAACATGCTTTGTGCAAGATTTTAAA 875
Db 1145 TTTTACGGAAGATTGCTCAGAGGAGTCTCTCAACATGCTTTGTGCAAGATTTTAAA 1204
Qy 876 GATCTGTGTTGATTTTTCAGATGATTAACATGATGGAAGAAAGCTGTGAATCTTACA 935
Db 1205 GATCTGTGTTGATTTTTCAGATGATTAACATGATGGAAGAAAGCTGTGAATCTTACA 1264
Qy 936 AAGAAAGTCTGGCTGATGATTTGAAAATCTCTAGAGTGGCTAGTAAAGTCTG 995
Db 1265 AAGAAAGTCTGGCTGATGATTTGAAAATCTCTAGAGTGGCTAGTAAAGTCTG 1324
Qy 996 AAGAAATTTGAAGAGCTCAGAGACCAAGTTAAATCCCTTTCTCAGGAATCTGTATGAA 1055
Db 1325 AAGAAATTTGAAGAGCTCAGAGACCAAGTTAAATCCCTTTCTCAGGAATCTGTATGAA 1384
Qy 1056 TTTATATGTCATTAATAGAGAACTTATGAAAGATCCGTCATCGCATGAGATGGCTAT 1115
Db 1385 TTTATATGTCATTAATAGAGAACTTATGAAAGATCCGTCATCGCATGAGATGGCTAT 1444
Qy 1116 TCATATGAAAAAGAGCAATGAAAAATTTGATCAGCAAAAAAGAAAGCTACAGTCCCATG 1175
Db 1445 TCATATGAAAAAGAGCAATGAAAAATTTGATCAGCAAAAAAGAAAGCTACAGTCCCATG 1504
Qy 1176 ACAAAATCTTCTTCTCTCTTACGGCTACTTACACCAATAGACTCTGAAAAATGGCCATC 1235
Db 1505 ACAAAATCTTCTTCTCTCTTACGGCTACTTACACCAATAGACTCTGAAAAATGGCCATC 1564
Qy 1236 AATAGATGGCTGGAGACACACCAAAAGTAAA 1266
Db 1565 AATAGATGGCTGGAGACACACCAAAAGTAAA 1595

RESULT 8

US-10-287-218-40
; Sequence 40; Application US/10287218
; Publication No. US20030198975A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
; APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.
; APPLICANT: BECHA, Shanya D.; BOROMSKY, Mark L.
; APPLICANT: BUFORD, Neil; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
; APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: HONCHELL, Cynthia D.; LAU, Preeti G.
; APPLICANT: LEE, Soo Yeun; LU, Dying; Alina M.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: REDDY, Roopa; SANDANMALA, Madhu, M.
; APPLICANT: TANG, Y. Tom; WALIA, Nalinder K.
; APPLICANT: WANG, Yu-mei, E.; WARREN, Bridget A.
; APPLICANT: XU, Yuming; YANG, Junming
; APPLICANT: YAO, Monique G.; YUE, Henry
; APPLICANT: ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: P1-0417 USA
; CURRENT APPLICATION NUMBER: US/10/287,218
; PRIOR APPLICATION NUMBER: PCT/US02/11152
; PRIOR FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/349,705
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/295,263
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/295,340
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/293,727
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/291,846

; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/291,662
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/287,228
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/286,820
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/283,294
; PRIOR FILING DATE: 2001-04-11
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030198975A1 7483131CB1
US-10-287-218-40

Query Match 70.3%; Score 894; DB 17; Length 1773;
Best Local Similarity 80.6%; Pred. No. 8,6e-250;
Matches 1186; Conservative 0; Mismatches 10; Indels 276; Gaps 1;

Qy 71 GCCCGCCCTCCGACGCTGTTTTCTTCAATTAAGAAATGTAAGTGAATTCACAC 130
Db 20 GCGGCGGTGCGGCGAGCGCTTTTCTTCAATTAAGAAATGTAAGTGAATTCACAC 79
Qy 131 ATTAGTGATCATGTGAGAGATGCAACTGTGTGCTTCTCTTTCCCTCTTGCTAC 190
Db 80 ATTAGTGATCATGTGAGAGATGCAACTGTGTGCTTCTCTTTCCCTCTTGCTAC 139
Qy 191 TTGCTCTTGGACAAACAATTCGCTGTACTGCTTGAAGTCTTAACTGACCA 250
Db 140 TTGCTCTTGGACAAACAATTCGCTGTACTGCTTGAAGTCTTAACTGACCA 199
Qy 251 TTGCTCATGAAGTTTCAACCTATGCTCTCCACTGCTCTGTTTCCCTTCAGACA 310
Db 200 TTGCTCATGAAGTTTCAACCTATGCTCTCCACTGCTCTGTTTCCCTTCAGACA 259
Qy 311 TATTTTGGCATGCTGTTCAACAGATGTAACACTGCTCTATGAAATATGAAATGACA 370
Db 260 TATTTTGGCATGCTGTTCAACAGATGTAACACTGCTCTATGAAATATGAAATGACA 319
Qy 371 GATGCTGGAGATGATGAACAGCTTATGTCAGACCTGTGAGAGGTTTGGCAATTTCCCC 430
Db 320 GATGCTGGAGATGATGAACAGCTTATGTCAGACCTGTGAGAGGTTTGGCAATTTCCCC 379
Qy 431 AGACTCCAGCTGTTGGCATCAGGGGACAGCTGATGGAACCTGTGTTGTGGAATGACA 490
Db 380 AGACTCCAGCTGTTGGCATCAGGGGACAGCTGATGGAACCTGTGTTGTGGAATGACA 439
Qy 491 GTCATTAACAATTATATAGATGTGTATGAATGCTCTCTTGGCGGATGTGCATT 550
Db 440 GTCATTAACAATTATATAGATGTGTATGAATGCTCTCTTGGCGGATGTGCATT 499
Qy 551 TTGCTCTAATGGAAGCTTTCTTGTCACTGCTCTTATGATGATTTTAAAGTGTGGA 610
Db 500 TTGCTCTAATGGAAGCTTTCTTGTCACTGCTCTTATGATGATTTTAAAGTGTGGA 559
Qy 611 TGATAAATGAGGTGCTCATAGTGAATAAGCAATGATCTTGGAAATTAACGCTGCGCA 670
Db 560 TGATAAATGAGGTGCTCATAGTGAATAAGCAATGATCTTGGAAATTAACGCTGCGCA 619
Qy 671 TTTTCTTCAAGCCAGTTTGTATGAGAGAACAGGTCTTCAAGTTTTCGACTGGCATC 730
Db 620 TTTTCTTCAAGCCAGTTTGTATGAGAGAACAGGTCTTCAAGTTTTCGACTGGCATC 679
Qy 731 ATGTGTCAGATTTGCCAAGTCAAAATTTGATTTGTTCTTTTAAACCATATCTT----- 784
Db 680 ATGTGTCAGATTTGCCAAGTCAAAATTTGATTTGTTCTTTTAAACCATATCTTAAAGTTT 739

QY 551 TTCTCTAATGAGAGCTTTCTTGTCACTGGCTCCTCATGHTGATTAACAGTGTGGG 610
| | | | |
Db 500 TTCTCTAATGAGAGCTTTCTTGTCACTGGCTCCTCATGHTGATTAACAGTGTGGG 559
| | | | |
QY 611 TGAATAAATGAGGTGTCTGCATAGTGAAGAAAAGACATGATCTTGAATTAACCTGTGGG 670
| | | | |
Db 560 TGAATAAATGAGGTGTCTGCATAGTGAAGAAAAGACATGATCTTGAATTAACCTGTGGG 619
| | | | |
QY 671 TTTTCTTCAACAGCCAGTTCTCATAGAGAAACAAGCTTCAATTTTGTGATCTGGCATC 730
| | | | |
Db 620 TTTTCTTCAACAGCCAGTTCTCATAGAGAAACAAGCTTCAATTTTGTGATCTGGCATC 679
| | | | |
QY 731 ATGTGTCAGAGATTGCCAATCAAAAATTGGATTGTTCTTTTACCATATCTT----- 784
| | | | |
Db 680 ATGTGTCAGAGATTGCCAATCAAAAATTGGATTGTTCTTTTACCATATCTTAGGTTT 739
| | | | |
QY 785 ----- 784
| | | | |
Db 740 TGAATTAATAATATAAAGTACACTGAGTGGGCACTGTGCTCTGTCTGTGCTTGTGCTTT 799
| | | | |
QY 785 ----- 784
| | | | |
Db 800 TTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGGATAGTCTGTCAATAGATATGA 859
| | | | |
QY 785 ----- 784
| | | | |
Db 860 TACTAATACTGAGATATACTTCACATTTGACTCAGACACACGAGTATGCAAACTTG 919
| | | | |
QY 785 ----- 784
| | | | |
Db 920 TGTCTTTCACCTAATACCTTTTACTGCTAGTGTCAATGAGCAAAAACAGTGAACAT 979
| | | | |
QY 785 ----- 814
| | | | |
Db 980 CTGGCAATTTGACCTGAGAAACATTTGCCAAGAGAGACACGAAATATAGCTGAAGCA 1039
| | | | |
QY 815 ATTTACCGAAGATTGCTCAGAGAGAGTCTCTCAACATGCTTTGTGCACAAAGATTAA 874
| | | | |
Db 1040 ATTTACCGAAGATTGCTCAGAGAGAGTCTCTCAACATGCTTTGTGCACAAAGATTAA 1099
| | | | |
QY 875 AGATCTTTGTTGTTTCAAGATGAATTAACATTGATGAAAAAAGAACTGTTGAATCTTAC 934
| | | | |
Db 1100 AGATCTTTGTTGTTTCAAGATGAATTAACATTGATGAAAAAAGAACTGTTGAATCTTAC 1159
| | | | |
QY 935 AAAAAGAAAGTCTGATGATTTGAAAAATGAAATCTAGCACTGGCTGATTAAGTCT 994
| | | | |
Db 1160 AAAAAGAAAGTCTGATGATTTGAAAAATGAAATCTAGCACTGGCTGATTAAGTCT 1219
| | | | |
QY 995 GAGAAAAATTGAAGCTCAGACCAAGGTTAAATCCCTTTCTTCAGAAATTCCTGATGA 1054
| | | | |
Db 1220 GAGAAAAATTGAAGCTCAGACCAAGGTTAAATCCCTTTCTTCAGAAATTCCTGATGA 1279
| | | | |
QY 1055 ATTTAATATGTCATTAATCTAGAGAACTTATGAAAAAGATCCGGTCAATCCATAGTGGCTA 1114
| | | | |
Db 1280 ATTTAATATGTCATTAATCTAGAGAACTTATGAAAAAGATCCGGTCAATCCATAGTGGCTA 1339
| | | | |
QY 1115 TTCAATGAAAAAGAAAGCAATGAAAAATTGATCAGCAAAAAAGAAAGCTCAAGTCCCAT 1174
| | | | |
Db 1340 TTCAATGAAAAAGAAAGCAATGAAAAATTGATCAGCAAAAAAGAAAGCTCAAGTCCCAT 1399
| | | | |
QY 1175 GACAAATCTTTGTTCTTCTTCAGCGGTACTTACACCAATAGGACTCTGAAAAATGGCCAT 1234
| | | | |
Db 1400 GACAAATCTTTGTTCTTCTTCAGCGGTACTTACACCAATAGGACTCTGAAAAATGGCCAT 1459
| | | | |
QY 1235 CATATAGTGGCTGAGACACACCAAAAGTAAA 1266
| | | | |
Db 1460 CATATAGTGGCTGAGACACACCAAAAGTAAA 1491
| | | | |

RESULT 10

US-10-104-047-1689
; Sequence 1689, Application US/10104047
; Publication No. US20030236392A1

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1689
; LENGTH: 1811
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1689

Query Match 70.0%; Score 890.2; DB 18; Length 1811;
Best Local Similarity 80.9%; Pred. No. 1.1e-248;
Matches 1178; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 86 GGCTGTTTTCTTCAATAAAGAAACATGAGTGAACATGATTCACACATTAAGCTGATG 145
| | | | |
Db 125 GGCTGTTTTCTTCAATAAAGAAACATGAGTGAACATGATTCACACATTAAGCTGATG 184
| | | | |
QY 146 TGAAGATGTCACAGTGTGCTGCTCTCTCTTCCCTTGGCTACTTGTGCTTGGACAA 205
| | | | |
Db 185 TGAAGATGTCACAGTGTGCTGCTCTCTCTTCCCTTGGCTACTTGTGCTTGGACAA 244
| | | | |
QY 206 AACAAATTCGCTGTACTCTGTACGTGACTTTTACTGAACAGCCATTTCTCATTTGAAGTT 285
| | | | |
Db 245 AACAAATTCGCTGTACTCTGTACGTGACTTTTACTGAACAGCCATTTCTCATTTGAAGTT 304
| | | | |
QY 266 TCATACCTATGCTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325
| | | | |
Db 305 TCATACCTATGCTGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
| | | | |
QY 326 TTCACAGATGATGATCACTGCTCTATGAAATCTGAAAAATGACAGATCTGGCAGTAT 385
| | | | |
Db 365 TTCACAGATGATGATCACTGCTCTATGAAATCTGAAAAATGACAGATCTGGCAGTAT 424
| | | | |
QY 386 GGAACAGCTAGTGGCAGCCCTGTGAGGTTTGGCCAGTTTCCCGACATCCAGTGTCTT 445
| | | | |
Db 425 GGAACAGCTAGTGGCAGCCCTGTGAGGTTTGGCCAGTTTCCCGACATCCAGTGTCTT 484
| | | | |
QY 446 GGCATAGGGGAGCGATGAGAACTGTGTTTTGAGAAATGCAATCATACAAATTTATA 505
| | | | |
Db 485 GGCATAGGGGAGCGATGAGAACTGTGTTTTGAGAAATGCAATCATACAAATTTATA 544
| | | | |
QY 506 TAGATGTGTAGTGTAAAGATGCTCTTGGCGCATGTGATTTTCTCTAATGGAAG 565
| | | | |
Db 545 TAGATGTGTAGTGTAAAGATGCTCTTGGCGCATGTGATTTTCTCTAATGGAAG 604
| | | | |
QY 566 CTTCCTTTGTCAGTGGCTCCTCATGTGTGATTTAACAAGTGTGGATGATTAATGAGGTG 625
| | | | |
Db 605 CTTCCTTTGTCAGTGGCTCCTCATGTGTGATTTAACAAGTGTGGATGATTAATGAGGTG 664
| | | | |
QY 626 TCTGCAATGAAAAAGCAATGATCTTGAATTTTACCTGCGATTTTCTTCAACAGCC 685
| | | | |
Db 665 TCTGCAATGAAAAAGCAATGATCTTGAATTTTACCTGCGATTTTCTTCAACAGCC 724
| | | | |
QY 686 AGTTTGTATGAGAAACAAGTCTTCAATTTTTCAGCTGCGCATCTCATGTGTGAGATTTG 745
| | | | |
Db 725 AGTTTGTATGAGAAACAAGTCTTCAATTTTTCAGCTGCGCATCTCATGTGTGAGATTTG 784
| | | | |
QY 746 CCAAGTCAAAATTTGATGTTTCTTTTACCATATCTT----- 784
| | | | |
Db 785 CCAAGTCAAAATTTGATGTTTCTTTTACCATATCTT----- 844
| | | | |
QY 785 ----- 784
| | | | |
Db 845 AAGTACACTGATGGGCACTGTGCTCTGCTTGTGCTTGTCTTTTCCCATGATGAGGCA 904
| | | | |
QY 785 ----- 784
| | | | |

Db 905 GATGCTAGTCTCAGGGTCAGTGAATAGTCTGTATATAGTACTAATACTAGAA 964
QY 785 ----- 784
Db 965 TATACTTCACACATTCGACGACACAGGTATGTCAACATTGCTTTTGCACCTAA 1024
QY 785 ----- 784
Db 1025 TACCTTTTACTTGCTACTGCTTCAATGACAAAACAGTGAACCTTGGCAATTGACCT 1084
QY 785 -----ACGAAGGCGCAGACAGAACATCAGCTGAAGCAATTTTACCGAAGATTG 829
Db 1085 GGAACACCTTGGCAGCAAGAGACAGACAGAACATCAGCTGAAGCAATTTTACCGAAGATTG 1144
QY 830 GTGAGAGAGAGGTGCTCTCAACATGCTTTGTGCAAGATTTTAAAGATCTTGTGGTAT 889
Db 1145 GTGAGAGAGAGGTGCTCTCAACATGCTTTGTGCAAGATTTTAAAGATCTTGTGGTAT 1204
QY 890 TTTCAAGATGAATTAACATTTGATGGAAGAAAGCTGTTGAATCTTACAAAGAGCTGGC 949
Db 1205 TTTCAAGATGAATTAACATTTGATGGAAGAAAGCTGTTGAATCTTACAAAGAGCTGGC 1264
QY 950 TGATGATTTGAAAATTGAATCTCTAGAGACTGCGTAGTAAAGTGTGAGAAAATTGAGA 1009
Db 1265 TGATGATTTGAAAATTGAATCTCTAGAGACTGCGTAGTAAAGTGTGAGAAAATTGAGA 1324
QY 1010 GCTCAGAGCAAGTTAAATCTCTTCTTCAAGAAATCTTGATGATTTATATGCTCAAT 1069
Db 1325 GCTCAGAGCAAGTTAAATCTCTTCTTCAAGAAATCTTGATGATTTATATGCTCAAT 1384
QY 1070 AACTAGAGAACTTGAAGATCCGGTCAATGCGATCGATGAGTCAATCAATGAAGAA 1129
Db 1385 AACTAGAGAACTTGAAGATCCGGTCAATGCGATCGATGAGTCAATCAATGAAGAA 1444
QY 1130 AGCAATGAAAATTGGATCAGCAAAAAGAAACGTACAGTCCCATGACAAATCTTGTCT 1189
Db 1445 AGCAATGAAAATTGGATCAGCAAAAAGAAACGTACAGTCCCATGACAAATCTTGTCT 1504
QY 1190 TCCTTCAGCGGTACTTACACCAATAGAGACTCTGAAAATGGCCATCAATGATGCTGGA 1249
Db 1505 TCCTTCAGCGGTACTTACACCAATAGAGACTCTGAAAATGGCCATCAATGATGCTGGA 1564
QY 1250 GACACACCAAAAGTAA 1266
Db 1565 GACACACCAAAAGTAA 1581

RESULT 11
US-10-357-930-23179
; Sequence 23179, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007

; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23179
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
; LOCATION: 1995, 1996
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-23179

Query Match 69.1%; Score 878.8; DB 21; Length 1996;
Best Local Similarity 80.7%; Pred. No. 2,6e-245;
Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1;

QY 99 CAATTAAGAAACATGGTGAACCTGATTCACACATTAAGTATGATGCTGACATGTCAC 158
Db 4 CAATTAAGAAACATGGTGAACCTGATTCACACATTAAGTATGATGCTGACATGTCAC 63
QY 159 TGCTGTCCTTCTCTCTTCT 218
Db 64 TGCTGTCCTTCTCTCTTCT 123
QY 219 TACTGTTAGTGAATTTTACTGAACTGCAATTTCTCATTAAGTTTCATTAACCTATGT 278
Db 124 TACTGTTAGTGAATTTTACTGAACTGCAATTTCTCATTAAGTTTCATTAACCTATGT 183
QY 279 GTCCACGTCGCTGCTTCT 338
Db 184 GTCCACGTCGCTGCTTCT 243
QY 339 ACCACTGTCCTATGAATACTGAATAATGACAGATGCTGAGTATGAAACAGCTAGT 398
Db 244 ACCACTGTCCTATGAATACTGAATAATGACAGATGCTGAGTATGAAACAGCTAGT 303
QY 399 GGCAGCCCTGAGAGGTTTCCAGTTTCCCAAGTCTCAGTGTGTCATCAGGGGCA 458
Db 304 GGCAGCCCTGAGAGGTTTCCAGTTTCCCAAGTCTCAGTGTGTCATCAGGGGCA 363
QY 459 GCTGATGGAACGTGCTTGTGGAATGACAGTCAATTAATTAATTAATTAATTAATTA 518
Db 364 GCTGATGGAACGTGCTTGTGGAATGACAGTCAATTAATTAATTAATTAATTAATTA 423
QY 519 GTTAAAGATGAGTCTCTTGGCGGATGTCATTTTCTCTAATGGAAGCTTCTTGTCACT 578
Db 424 GTTAAAGATGAGTCTCTTGGCGGATGTCATTTTCTCTAATGGAAGCTTCTTGTCACT 483
QY 579 GGCCTCTCATGTGATGATTTTAAAGTGGGATGATTAATTAATTAATTAATTAATTA 638
Db 484 GGCCTCTCATGTGATGATTTTAAAGTGGGATGATTAATTAATTAATTAATTAATTA 543
QY 639 AAAGCAGATATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 698
Db 544 AAAGCAGATATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 603
QY 699 GAACAAGTCTTCAAGTTTTCAGTCACTGCAATGATGATGATGATGATGATGATGATGAT 758
Db 604 GAACAAGTCTTCAAGTTTTCAGTCACTGCAATGATGATGATGATGATGATGATGATGAT 663
QY 759 TGATTTGTTCTTTTACCAATTTCTT----- 784
Db 664 TGATTTGTTCTTTTACCAATTTCTT----- 723
QY 785 ----- 784
Db 724 GGGCAGTGTGCTCTGTTGCTGCTGCTGCTTTCCTCATGATGGCAGATGCTAGTCTCA 783
QY 785 ----- 784

Db 784 GGGTCAGTGAATAGTCTGATAGTATATAGTACTAATACTGAGATATATTCTTACACA 843
QY 785 ----- 784
Db 844 TTGACTACGACACCAAGTATGTCAACAATTGTGCTTTTGACCTAATACCTTTTACTT 903
QY 785 ----- 784
Db 904 GCTACTGTTTCAATGACAAACAGTGAACATCTGGCAATTGACCTGGAACACTTTTGC 963
QY 785 --AGCAAGGCGCACAGAACATCACTGAGCAATTTACGGAAGTTGCTCAGAGAGCTC 842
Db 964 CAAGCAAGGCGCACAGAACATCACTGAGCAATTTACGGAAGTTGCTCAGAGAGAGAT 1023
QY 843 GTCTCAACATGGCTTTGTGACAAAGATTTAAAGATCTTGTGATTTTTCAGATGAAT 902
Db 1024 GTCTCAACATGGCTTTGTGACAAAGATTTAAAGATCTTGTGATTTTTCAGATGAAT 1083
QY 903 AACATTGATGAAAGAAAGATGTTGAATCTTACAAAAGAAAGCTGGCTGATGATTTGAA 962
Db 1084 AACATTGATGAAAGAAAGATGTTGAATCTTACAAAAGAAAGCTGGCTGATGATTTGAA 1143
QY 963 ATTGAATCTCTAGAGACTGCGTGTAGTAAAGTGTGAGGAAATTTGAAGACTCAGGACCA 1022
Db 1144 ATTGAATCTCTAGAGACTGCGTGTAGTAAAGTGTGAGGAAATTTGAAGACTCAGGACCA 1203
QY 1023 GTTAAATCCCTTTCTTCAGGAATTTCTGAGATTTTATATGTCATTAATTAAGAACTT 1082
Db 1204 GTTAAATCCCTTTCTTCAGGAATTTCTGAGATTTTATATGTCATTAATTAAGAACTT 1263
QY 1083 ATGAAAGATCCGCTCATTCGATCAGATGAGTATTCATATGAAAGAAAGCAATGAGAAAT 1142
Db 1264 ATGAAAGATCCGCTCATTCGATCAGATGAGTATTCATATGAAAGAAAGCAATGAGAAAT 1323
QY 1143 TGGATCAGCAAAAAGAAAGTACAGTCCCATGACAAATTTTCTTCTTCAAGCGGTA 1202
Db 1324 TGGATCAGCAAAAAGAAAGTACAGTCCCATGACAAATTTTCTTCTTCAAGCGGTA 1383
QY 1203 CTTCACCAAAATGAGACTCTGAAATAGGCCATGATAGATGCTGGAGACACCAAAAG 1262
Db 1384 CTTCACCAAAATGAGACTCTGAAATAGGCCATGATAGATGCTGGAGACACCAAAAG 1443
QY 1263 TAAA 1266
Db 1444 TAAA 1447

RESULT 12
US-10-357-930-29046
Sequence 29046, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlögel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357, 930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785, 276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183, 319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189, 862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207, 454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211, 314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219, 007

QY 99 CAAATAAGAACATGGTGAACATGATTCAACATTAAGTATGATGATGATGATGATGATGAT 158
Db 4 CAAATAAGAACATGGTGAACATGATTCAACATTAAGTATGATGATGATGATGATGATGAT 63
QY 159 TGCTGTGCTTCT 218
Db 64 TGCTGTGCTTCT 123
QY 219 TACTGTTACGTACCTTTTACTGACATGACATGACATGACATGACATGACATGACATGAC 278
Db 124 TACTGTTACGTACCTTTTACTGACATGACATGACATGACATGACATGACATGACATGAC 183
QY 279 GTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 338
Db 184 GTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY 339 ACCATGCTCTATGAAATCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 398
Db 244 ACCATGCTCTATGAAATCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 303
QY 399 GCGAGCCCTGTAGGGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGTGT 458
Db 304 GCGAGCCCTGTAGGGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGTGT 363
QY 459 GCTGATGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 518
Db 364 GCTGATGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
QY 519 GTTAAAGATGCTCTTGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
Db 424 GTTAAAGATGCTCTTGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
QY 579 GGCTCTCATGCGGATTTTAAACAGTGTGGAATGAAATGAGTGTGCTGATGAA 638
Db 484 GGCTCTCATGCGGATTTTAAACAGTGTGGAATGAAATGAGTGTGCTGATGAA 543
QY 639 AAAGCATGATCTTGAATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698
Db 544 AAAGCATGATCTTGAATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
QY 699 GAAAGAGTCTTCAAGTTTTCAGTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
Db 604 GAAAGAGTCTTCAAGTTTTCAGTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
QY 759 TGGATTGTTCTTTTAAACCATATCTT----- 784
Db 664 TGGATTGTTCTTTTAAACCATATCTTAAAGTTGAATTAATAAAGTACATGAGT 723
QY 785 ----- 784
Db 724 GGGCACTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
QY 785 ----- 784

PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255, 281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PaedSeq for Windows Version 4.0
SEQ ID NO 29046
LENGTH: 1996
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
LOCATION: 1995, 1996
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-29046

Query Match 69.1%; Score 878.8; DB 21; Length 1996;
Best Local Similarity 80.7%; Pred. No. 2,6e-245;
Matches 1166; Conservative 0; Mismatches 2; Indels 276; Gaps 1;

Db 784 GGGTCAGTGGATAGTCTGTGATAGTATAGTACTAATACTGAGAAATATCTTACACACA 843
Qy 785 ----- 784
Db 844 TTGACTCAGCACACAGGATATGTCAACAATTGTCTTTTGACCTAAATACCCTTTTACTT 903
Qy 785 ----- 784
Db 904 GCTACTGCTTCAATGACACAAAACAGTGAACATCTGGCAATTTGACTTGGAAACCTTTGC 963
Qy 785 --AGCAAGGGCGACAGAAATCAGCTGAGCAATTTTCCGAAGATTGGTCAGAGAGATC 842
Db 964 CAAGCAAGGGCGACAGAAATCAGCTGAGCAATTTTCCGAAGATTGGTCAGAGAGAT 1023
Qy 843 GTCTCAACATGAGCTTTGTGCAAGAAATTTAAAGATCTTGTGGTATTTTCAAGATGAT 902
Db 1024 GTCTCAACATGAGCTTTGTGCAAGAAATTTAAAGATCTTGTGGTATTTTCAAGATGAT 1083
Qy 903 AACATTGATGGAAGAAAGCTGTAATCTTACAAAAGAAAGCTGGCTGATGATTTGAAA 962
Db 1084 AACATTGATGGAAGAAAGCTGTAATCTTACAAAAGAAAGCTGGCTGATGATTTGAAA 1143
Qy 963 ATTGAATCTCTAGAGACTGCGTAGTAAAGTCTGAGAAATTTGAAGCTCAGAGCAAG 1022
Db 1144 ATTGAATCTCTAGAGACTGCGTAGTAAAGTCTGAGAAATTTGAAGCTCAGAGCAAG 1203
Qy 1023 GTTAAATCCCTTTCTTCAAGAAATCTGATGATTTTATATGCTCAATTAAGTAACTT 1082
Db 1204 GTTAAATCCCTTTCTTCAAGAAATCTGATGATTTTATATGCTCAATTAAGTAACTT 1263
Qy 1083 ATGAAATATCCGCTCATCGCATCGCATGAGCTATCATATGAAAGAAAGCAATGAAAT 1142
Db 1264 ATGAAATATCCGCTCATCGCATCGCATGAGCTATCATATGAAAGAAAGCAATGAAAT 1333
Qy 1143 TGGATCAGCAAAAAGAAAGCTGCAAGTCCCATGCAAAATCTTCTTCCCTTACGGGTA 1202
Db 1324 TGGATCAGCAAAAAGAAAGCTGCAAGTCCCATGCAAAATCTTCTTCCCTTACGGGTA 1383
Qy 1203 CTTACACCAATATAGGACTCTGCAAAATGCGCATCAATATGATGGCTGAGACACACCAAAAG 1282
Db 1384 CTTACACCAATATAGGACTCTGCAAAATGCGCATCAATATGATGGCTGAGACACACCAAAAG 1443
Qy 1263 TAAA 1266
Db 1444 TAAA 1447

RESULT 13

US-10-077-111-14
; Sequence 14, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Todderud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jili
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-4114US2
; CURRENT APPLICATION NUMBER: US/10/077,111
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: RET 16.3 splice variant
US-10-077-111-14

Query Match 69.0%; Score 877.8; DB 14; Length 1908;
Best Local Similarity 77.9%; Pred. No. 4,9e-245;
Matches 1253; Conservative 0; Mismatches 2; Indels 354; Gaps 2;
Qy 12 TCACCTGCGGCGACGATGACCCGACCGCCGTCGAGCCTTGAAGCGGATCCCGCG 71
Db 37 TCACCTGCGGCGACGATGACCCGACCGCCGTCGAGCCTTGAAGCGGATCCCGCG 96
Qy 72 CCCCCGCTCTCGCAGGCTGTTTTTCTTCAATTAAGAACTGTTGAATCTGATTCACACA 131
Db 97 CCCCCGCTCTCGCAGGCTGTTTTTCTTCAATTAAGAACTGTTGAATCTGATTCACACA 156
Qy 132 TTAGCTGATGATGTCGATGTCACATGTCAGTGCCTTCCCTTCCCTTCCCTTCCCTTCC 191
Db 157 TTAGCTGATGATGTCGATGTCACATGTCAGTGCCTTCCCTTCCCTTCCCTTCCCTTCC 216
Qy 192 TGCTCTTGGACAAACAAATTCGCTGATCTGTTACGTGATCTTGAATGATGACAT 251
Db 217 TGCTCTTGGACAAACAAATTCGCTGATCTGTTACGTGATCTTGAATGATGACAT 276
Qy 252 TCTTCATTTGAAGTTTCACTTACCTATGCTGTCACCTGCTGCTGTTTCTCCCTTCAAGCAT 311
Db 277 TCTTCATTTGAAGTTTCACTTACCTATGCTGTCACCTGCTGCTGTTTCTCCCTTCAAGCAT 336
Qy 312 ATTTTGGCATGCTGTTCAACAGATGTAACACATGTAACATGCTGATGATGATGATGATGAT 371
Db 337 ATTTTGGCATGCTGTTCAACAGATGTAACACATGTAACATGCTGATGATGATGATGATGAT 396
Qy 372 ATGCTGCACTGATGTAACAGCTAGTGGAGCCCTGTCAGAGGTTTGGCCAGTTTCCCA 431
Db 397 ATGCTGCACTGATGTAACAGCTAGTGGAGCCCTGTCAGAGGTTTGGCCAGTTTCCCA 456
Qy 432 GACTCCAGCTGTTGGCATGAGGCGCAGCTGATGAACTGTGTTTGGAAATGACAG 491
Db 457 GACTCCAGCTGTTGGCATGAGGCGCAGCTGATGAACTGTGTTTGGAAATGACAG 516
Qy 492 TCATACAAATTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
Db 517 TCATACAAATTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
Qy 552 TCTCTTAATGGAAGCTTCTTGTCTACTGCTCTCATGATGATGATGATGATGATGATGAT 611
Db 577 TCTCTTAATGGAAGCTTCTTGTCTACTGCTCTCATGATGATGATGATGATGATGATGAT 636
Qy 612 GATTAATATGAGGTCTGCAATGTAAGAAAGCAATATCTTGAATTTACCTGTCGAT 671
Db 637 GATTAATATGAGGTCTGCAATGTAAGAAAGCAATATCTTGAATTTACCTGTCGAT 696
Qy 672 TTTTCTTCAAGCAGCTTCTGATGAGAAACAAGGCTTCAAGTTTTCGACTGGCATCA 731
Db 697 TTTTCTTCAAGCAGCTTCTGATGAGAAACAAGGCTTCAAGTTTTCGACTGGCATCA 756
Qy 732 TGTGTCAGATGTCAGCAAGTCAAAATTTGATTTCTTTTACCATATCTTAAGTTT 784
Db 757 TGTGTCAGATGTCAGCAAGTCAAAATTTGATTTCTTTTACCATATCTTAAGTTT 816
Qy 785 ----- 784
Db 817 GAATTAATAATATAAAGTACAGTGAAGGACAGTGTCTCTCTTCTGCTTGTCTTTT 876
Qy 785 ----- 784
Db 877 TCCCATGATGGCAGATGCTAGTCTCAGGGTCAAGTGAATAGTCTGTCATATATATGAT 936
Qy 785 ----- 784
Db 937 ACTAATAGTGAATATATCTTACACATGATGATGACACACAGGATATGTCACAACTTGT 996
Qy 785 ----- 784
Db 997 GCTTTTGACCTATATACCTTTTACTTGTCTAGTGTTCATATGACAAACAGTGAACATC 1056

QY 785 -----AGCAAGCGCAGAAACATCAGTGAAGCAA 815
Db 1057 TGGCAATTTGACCTGGAAACCTTTGGCAAGCAAGGGGCAACAGACATCGAGTGAAGCAA 1116
QY 816 TTTTACCGAAGATTGGTCAGAGAGGCTGTCTCAACATGGCTTTGTGCAACAAGTTTAAAA 875
Db 1117 TTTTACCGAAGATTGGTCAGAGAGGCTGTCTCAACATGGCTTTGTGCAACAAGTTTAAAA 1176
QY 876 GATCTGTGTGATTTTTCAGATGAATTAACATGATGGAAGAAAGACTGTGAATCTTACA 935
Db 1177 GATCTGTGTGATTTTTCAGATGAATTAACATGATGGAAGAAAGACTGTGAATCTTACA 1236
QY 936 AAGAAAGCTGGCTGATGATTTTGAATTTG----- 966
Db 1237 AAGAAAGCTGGCTGATGATTTTGAATTTGCGTGAAGTCTGTGGCATGTGATGCTC 1296
QY 967 -----AATCTTAAGA 977
Db 1297 ACTGACGCTTCAACCTCTGGGCTCAAGTATCTCTCACTCGGCTCAATCTTAAGA 1356
QY 978 CTGCTAGTAAAGTGTGAGAAATTTGAAGAGCTCAGACCAAGGTTAAATCGCTTCT 1037
Db 1357 CTGCTAGTAAAGTGTGAGAAATTTGAAGAGCTCAGACCAAGGTTAAATCGCTTCT 1416
QY 1038 TCAGAAATTCCTGATGAATTTATATGTCAATAAATAAGAACTTATGAAGATCCGCTC 1097
Db 1417 TCAGAAATTCCTGATGAATTTATATGTCAATAAATAAGAACTTATGAAGATCCGCTC 1476
QY 1098 ATGGCATCAGATGCTTATCTATATGAAGAAAGCAATGGAATTTGATCAGCAAAAG 1157
Db 1477 ATGGCATCAGATGCTTATCTATATGAAGAAAGCAATGGAATTTGATCAGCAAAAG 1536
QY 1158 AAACGTACAAGTCCCATGACAAATCTGTCTTCTTCAAGGTACTTACACCAATAGG 1217
Db 1537 AAACGTACAAGTCCCATGACAAATCTGTCTTCTTCAAGGTACTTACACCAATAGG 1596
QY 1218 ACTCTGAATAATGGCCATCAATGAATGGCTGGAGACACCAAAAGTAA 1266
Db 1597 ACTCTGAATAATGGCCATCAATGAATGGCTGGAGACACCAAAAGTAA 1645

RESULT 14
US-10-956-157-10363
; Sequence 10363, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 2004-10-04
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10363
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10363

Query Match 47.3%; Score 602.2; DB 22; Length 1400;
Best Local Similarity 76.1%; Pred. No. 1,4e-164;
Matches 890; Conservative 0; Mismatches 3; Indels 276; Gaps 1;

QY 374 GCTGGAGATGATGAACAGGCTAGTGGACGCTGTGAGGGTTTGGCAGTTTCCCGACA 433
Db 1 GCTGGAGATGATGAACAGGCTAGTGGACGCTGTGAGGGTTTGGCAGTTTCCCGACA 60
QY 434 CTCACGATGTTGGCATTCAGGGCAGCTGATGGAATGTGTTTGTGAATGACAGTGC 493
Db 61 CTCACGATGTTGGCATTCAGGGCAGCTGATGGAATGTGTTTGTGAATGACAGTGC 120

QY 494 ATCAATATATATAGATGTGATGTTTAAAGATGCTCTTGGCGGATGTCATTTTC 553
Db 121 ATCAATATATATAGATGTGATGTTTAAAGATGCTCTTGGCGGATGTCATTTTC 180
QY 554 TCCTAATGGAAGCTTTTGTGCACTGGCTCTCATGTGTGATTTTAACTGTGGATGA 613
Db 181 TCCTAATGGAAGCTTTTGTGCACTGGCTCTCATGTGTGATTTTAACTGTGGATGA 240
QY 614 TAAATGAGGTGTCTGATAGTGAAGAAACATGATCTTGGAAATTAACGCTGCGATTC 673
Db 241 TAAATGAGGTGTCTGATAGTGAAGAAACATGATCTTGGAAATTAACGCTGCGATTC 300
QY 674 TTCTTCAACCCAGTTTCTGATGAGAAACAGGCTCTTCAATTTTTCGACTGGCATCATG 733
Db 301 TTCTTCAACCCAGTTTCTGATGAGAAACAGGCTCTTCAATTTTTCGACTGGCATCATG 360
QY 734 TGGTCAGATTTGCAAGTCAAAATTTGATTTTCTTTTACCATATCTT----- 784
Db 361 TGGTCAGATTTGCAAGTCAAAATTTGATTTTCTTTTACCATATCTTAGTTTGA 420
QY 785 ----- 784
Db 421 ATTTAAATTTAAAGTACATGAGTGGCACTGTGCTCTGTGCTTGGCTTTGCTTTTC 480
QY 785 ----- 784
Db 481 CCATGATGGCAGATGCTAGTCTCAGAGGTCAGTGATTAATCTGTCAATGATATGATAC 540
QY 785 ----- 784
Db 541 TAATAGTAATATATCTTACACATTTGACTCAGCACACAGGTATGTCAAACTTGTGC 600
QY 785 ----- 784
Db 601 TTTTGCACTAATACCTTTTACTTGCTCTGTGTTCAATGAGAAACAGTGAACATTC 660
QY 785 -----AGCAAGCGCAGCAAGAACATCAGCTGAAGCAAT 817
Db 661 GCAATTTGACCTGGAACACATTTGCCAACAGGGCGCACAGAACATCAGCTGAAGCAAT 720
QY 818 TACCGAAGATTTGTCAGAGAGGTGCTTCAACATGGCTTTTGTGCAACAAGTTTAAAGA 877
Db 721 TACCGAAGATTTGTCAGAGAGGTGCTTCAACATGGCTTTTGTGCAACAAGTTTAAAGA 780
QY 878 TCTTGTGATTTTAAAGATGAATTAACATTTGATGGAAGAAAGTGTGAATCTTACAA 937
Db 781 TCTTGTGATTTTAAAGATGAATTAACATTTGATGGAAGAAAGTGTGAATCTTACAA 840
QY 938 AGAAGTCTGGCTGATGATTTGAAATTTGAATCTCTAGACTGCGTAGTAAAGTGTGAG 997
Db 841 AGAAGTCTGGCTGATGATTTGAAATTTGAATCTCTAGACTGCGTAGTAAAGTGTGAG 900
QY 998 GAAATTTGAAGAGCTCAGAACCAAGTTAAATCCCTTTCTTCAAGAAATCTCTGATGAAT 1057
Db 901 GAAATTTGAAGAGCTCAGAACCAAGTTAAATCCCTTTCTTCAAGAAATCTCTGATGAAT 960
QY 1058 TATATGCAATTAACAGAACTTATGAAGATCCGCTCATGCAATCAGATGCTATTC 1117
Db 961 TATATGCAATTAACAGAACTTATGAAGATCCGCTCATGCAATCAGATGCTATTC 1020
QY 1178 AAATCTTGTCTTCTTCAAGCGGTACTTACACCAATTTGAGCTGTGAANAATGCCATCA 1237
Db 1081 AAATCTTGTCTTCTTCAAGCGGTACTTACACCAATTTGAGCTGTGAANAATGCCATCA 1140
QY 1238 TAGATGCTGAGACACACCAAAAGTAA 1266
Db 1141 TAGATGCTGAGACACACCAAAAGTAA 1169

Query	Match	Best Local Similarity	Score	DB	Length
US-10-077-111-6	Sequence 6, Application US/10077111	63.2%	464	14	1901
US-10-077-111-6	Publication No. US20020187492A1				
US-10-077-111-6	GENERAL INFORMATION:				
US-10-077-111-6	APPLICANT: Toddlerud, C. Gordon				
US-10-077-111-6	APPLICANT: Finger, Joshua N.				
US-10-077-111-6	APPLICANT: Rillema, Jill				
US-10-077-111-6	TITLE OF INVENTION: TBA				
US-10-077-111-6	FILE REFERENCE: 3053-414US2				
US-10-077-111-6	CURRENT APPLICATION NUMBER: US/10/077,111				
US-10-077-111-6	CURRENT FILING DATE: 2002-02-15				
US-10-077-111-6	PRIOR APPLICATION NUMBER: 60/294,181				
US-10-077-111-6	PRIOR FILING DATE: 2001-05-29				
US-10-077-111-6	PRIOR APPLICATION NUMBER: 60/269,366				
US-10-077-111-6	PRIOR FILING DATE: 2001-02-16				
US-10-077-111-6	NUMBER OF SEQ ID NOS: 25				
US-10-077-111-6	SOFTWARE: PatentIn Ver. 2.1				
US-10-077-111-6	SEQ ID NO 6				
US-10-077-111-6	LENGTH: 1901				
US-10-077-111-6	TYPE: DNA				
US-10-077-111-6	ORGANISM: MOUSE				
US-10-077-111-6	Matches 916; Conservative 0; Mismatches 255; Indels 279; Gaps 2				
Query	Match	Best Local Similarity	Score	DB	Length
US-10-077-111-6	Sequence 6, Application US/10077111	63.2%	464	14	1901
US-10-077-111-6	Publication No. US20020187492A1				
US-10-077-111-6	GENERAL INFORMATION:				
US-10-077-111-6	APPLICANT: Toddlerud, C. Gordon				
US-10-077-111-6	APPLICANT: Finger, Joshua N.				
US-10-077-111-6	APPLICANT: Rillema, Jill				
US-10-077-111-6	TITLE OF INVENTION: TBA				
US-10-077-111-6	FILE REFERENCE: 3053-414US2				
US-10-077-111-6	CURRENT APPLICATION NUMBER: US/10/077,111				
US-10-077-111-6	CURRENT FILING DATE: 2002-02-15				
US-10-077-111-6	PRIOR APPLICATION NUMBER: 60/294,181				
US-10-077-111-6	PRIOR FILING DATE: 2001-05-29				
US-10-077-111-6	PRIOR APPLICATION NUMBER: 60/269,366				
US-10-077-111-6	PRIOR FILING DATE: 2001-02-16				
US-10-077-111-6	NUMBER OF SEQ ID NOS: 25				
US-10-077-111-6	SOFTWARE: PatentIn Ver. 2.1				
US-10-077-111-6	SEQ ID NO 6				
US-10-077-111-6	LENGTH: 1901				
US-10-077-111-6	TYPE: DNA				
US-10-077-111-6	ORGANISM: MOUSE				
US-10-077-111-6	Matches 916; Conservative 0; Mismatches 255; Indels 279; Gaps 2				

Db	658	AAACTCTGGGCTGTACTATTACCCGTCGTCTTAGGCTTTGAATTAAATATAAAGACA	717
QY	785	-----	784
Db	718	CTAAGTGGGCACTGCGCCCTGTTCTTGAGCTGTGCTTTTCACATGATGMAATGCTT	777
QY	785	-----	784
Db	778	GCATCGGGGTCAATGATTAATCTGTCATCATACATGATATCGGCCCTCAGAGTGTGTA	837
QY	785	-----	784
Db	838	CACACGCTGACTCAGCATACCAGGTATGTTACGACTTGTGCTTTGACACCACTCTC	897
QY	785	-----	784
Db	898	TTTACTTGCTACTGTTGTCATGACACAGTGAACATTTGGCAGTTTGACCTGGAAACA	957
QY	785	-----	836
Db	958	CCTTGCCAAACAGGAAACATGAACGACCCGCTGAACATTTCACCTGAAGATGCTCAG	1017
QY	837	GAGGTCTCTCAACATGGCTTTGTCACAAGATTTAAGAATCTTGTGGATTTTCAAG	896
Db	1018	GAGATGTCTCCGTGTGGCTTGTGCTCAAGGCTTGGAAAGCTTCGTGATTTTCAGC	1077
QY	897	ATGATTAACATTTGATGGAAAGAACTGTGAATCTTCACAAAGAAAGCTGCGTATGAT	956
Db	1078	GCAAAACAACATCGATGGAAAGAACTATTGCAATTCACAAAGAAAGCTGCGTATGAT	1137
QY	957	TTGAAATTTGAATCTCTAGGACTGCGTAGTAAAGTCTGAGAAATTTGAAGACTCAGG	1016
Db	1138	TTGAAATTCGAATCTCTAGGACTGCGAGCAAAAGTCTGAGAGTATTTGAAGACTCAGG	1197
QY	1017	ACCAAGGTTAAATCCCTTTCTTCAGGAATTCGTGATGAATTTATATGCTCAATTAACAGA	1076
Db	1198	GCCAAAGTGGATTCCTCTCTCTCCGGAATCCCTGACAGTTCATCTCCCAATTAACAGA	1257
QY	1077	GAACTTTGAAAGATCGGTCATCGGTCATCGATCGATGAGTGGTATTCATATGAAAGGAAGCAATG	1136
Db	1258	GAACTTCATGAAAGGCCCCGTCATCTGATTCAGATGCGATCTCTAGAGAGAGAAAGCAATG	1317
QY	1137	GAAATTTGATTCAGCAAAAGAAAGCAAGTACAGTCCATGACAAATCTTGTTCTTCTCTTCA	1196
Db	1318	GAAAGCTGATTCACACAGAAAGAACGTAACGAGCCCACTGACAAATTTGGCTCTCTCTTCA	1377
QY	1197	GCGGTACTTACACCAATTAGGACTCTGAAAATGCGCATCAATAGATGGCTGAGACACAC	1256
Db	1378	CTGGTACTGACCCCAACAGGACACTGAMAGATGGCCATCAACGATGGCTGAGAGCCAC	1437
QY	1257	CAAAAGTAAA 1266	
Db	1438	GAGAAATGAA 1447	

Search completed: October 25, 2005, 11:11:25
Job time : 2690 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 01:02:43 ; Search time 2816 Seconds
(without alignments)
5190.582 Million cell updates/sec

Title: US-10-077-111-13

Perfect score: 2047
Sequence: 1 MKLHHTLADHGDVNCACAF.....LTPRTIKMAINRWLETHQK 384

Scoring table:

BLOSUM62	
Xgapop 10.0, Xgapext 0.5	
Fgapop 10.0, Fgapext 0.5	
Delop 6.0, Delext 7.0	

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=20 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US10077111.@CGN_1_1.2607.@runat_24102005.072846.8180 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1977	96.6	1770	3	CR607851 full-length
2	1714.5	83.8	1600	3	CR619104 full-length
3	1617	79.0	2027	3	AK011391 Mus muscu
4	1205	58.9	889	1	AL553333 AL553333
5	1203	58.8	941	1	AL533510 AL533510
6	1154	56.4	1010	4	BMS43484 AGENCOURT
7	1043.5	51.0	858	4	B1603184 AGENCOURT
8	1031.5	50.4	792	4	B1821143 B03035030
9	1005	49.1	728	7	CN793033 4127990 B

10	975.5	47.7	910	5	B0895162
11	943.5	46.1	838	4 <td>B1107478</td>	B1107478
12	907	44.3	839	7 <td>CK306752</td>	CK306752
13	883.5	43.2	808	7 <td>CK792250</td>	CK792250
14	880	43.0	499	5 <td>BX282729</td>	BX282729
15	880	43.0	696	4 <td>B1759505</td>	B1759505
16	879	42.9	727	7 <td>CK64577</td>	CK64577
17	873	42.6	505	1 <td>AI189142</td>	AI189142
18	872	42.6	807	1 <td>AL040518</td>	AL040518
19	856.5	41.8	817	5 <td>B0961462</td>	B0961462
20	854	41.7	718	5 <td>B0356767</td>	B0356767
21	834	40.7	652	2 <td>B8653743</td>	B8653743
22	821	40.1	669	1 <td>AJ726222</td>	AJ726222
23	801	39.1	869	5 <td>B1148588</td>	B1148588
24	797	38.9	760	5 <td>B0273077</td>	B0273077
25	758.5	37.1	965	4 <td>BG769613</td>	BG769613
26	758	37.0	683	6 <td>CD215933</td>	CD215933
27	747	36.5	919	5 <td>BQ713478</td>	BQ713478
28	746	36.4	791	7 <td>CK603751</td>	CK603751
29	739	36.1	682	6 <td>BY710675</td>	BY710675
30	725	35.4	768	7 <td>CK846814</td>	CK846814
31	719	35.1	559	1 <td>B1681850</td>	B1681850
32	715	34.9	967	1 <td>AL533462</td>	AL533462
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36	691	33.8	723	9 <td>CE887278</td>	CE887278
37	690	33.7	632	4 <td>B0624489</td>	B0624489
38	677	33.1	626	4 <td>BG562985</td>	BG562985
39	673.5	32.9	447	1 <td>AA118718</td>	AA118718
40	668.5	32.7	1042	4 <td>BG435096</td>	BG435096
41	662.5	32.4	829	7 <td>CO567478</td>	CO567478
42	662	32.3	463	7 <td>CN407189</td>	CN407189
43	662	32.3	897	5 <td>B0964199</td>	B0964199
44	657	32.1	1010	3 <td>BC039804</td>	BC039804
45	648	31.7	699	1 <td>AJ726210</td>	AJ726210

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Full-length cDNA clone CS0DN004Y15 of Adult brain of Homo sapiens (human).
ACCESSION CR607851 GI:5048658
VERSION CR607851.1
KEYWORDS HTC, CNSLT CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1770)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@litech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1770)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. 1770
/organism="Homo sapiens"

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/cclone="CSDN004YJ15"
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Best Local Similarity:	80.25%
Query Match:	96.58%
DB:	3
Length:	177
Matches:	382
Conservative:	0
Mismatches:	2
Indels:	92
Gaps:	1

2.93e-190 Length: 1770

1977.00	Matches:	382
80 353	Conservative:	0

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80.25% CONSERVATIVE: V  
Mismatches: 2
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96.58%	Indels:	92
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Gaps:		

US-10-077-111-13 (1-384) x CR607851 (1-1770)

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Db	168	ATGGGAAACATCGATTCCACACATTAAGCTATCATGTGTGACGATGTCACATCGCTGTGCCTTC	227
QY	21	ScrPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg	40
Db	228	TCCTTTTCCCTCTTGCTTACCTTGCTCCCTTGGCAAAACATTCGCGCTTACCTCGTTACGT	287
QY	41	AspPheThrArgLeuLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys	60
Db	288	GACCTTACTGGAACCTGCACATCTCCATTCGATGGAAGTTTCATACCTTAAGCTGCACATCGCTGC	347
QY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	348	TGTTTCTCCCTTCAGACATATTTTGGCATGTGTCTTCAACAGATGATACCATGTCTCTA	407
QY	81	TrpAsnThrArgLeuAsnGlyGlnMetLeuAlaValMetGlnGlnProSerGlySerProVal	100
Db	408	TGGAAATACGAAAAATGGACAGATCTCTGCACAGTGAAGAAACGCTTAAGTGGACGCTGTG	467
QY	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr	120
Db	468	AGGGTTTGCCAGTTTCCCAACACTCCACGATGTTTGGCATCAGGGGGCAGCTGATGAACT	527
QY	121	ValValLeuThrTrpAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly	140
Db	528	GTGGTTTGTGGAAATGACACAGTCATACAAATATATATAGATGTGATGTTTAAAGATGGC	587
QY	141	SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	588	TCCCTGGGGGAGTGGCAATTTTCTCTAATGGAACCTTTTGTGCATCGGCTCCCACTGT	647
QY	161	GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp	180
Db	648	GGTGATTTTAAACAGTGTGGGATGATTAATGAATGAGTGTCCGCATATGTAAGAAAAGCATATAT	707
QY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu	200
Db	708	CTTGGAAATTAACCTGCTGGCATTTTCTTCACAGCAGATTTCTGAAGGAGAAACAAGTCTT	767
QY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrPheAlaSer	220
Db	768	CAGTTTTCATCGCGCATCATATGTTGTGAGATGGCAAGTCMAAATTTGGATGTTTCT	827
QY	221	PheThrHisIleLeu-----	225
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QY	225	-----	225
Db	888	CCTGTTCTGGCTGTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGGAT	947
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Percent Similarity: 70.38% Conservative: 0
Best Local Similarity: 70.38% Mismatches: 2
Query Match: 83.76% Indels: 139
Gaps: 2

US-10-077-111-13 (1-384) x CR619104 (1-1600)

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21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleGlyLeuTyrSerLeuArg 40
172 TCCCTTTCCTCTGCTGCTACTTGTCTTGGACAAACAATTCGCTGCTGCTTACGT 231
41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaIleHisCys 60
232 GACTTTTACTGACGTCACATTCCTCATTAAGTTTCACTTACCTGCTGCTGCTGCTG 291
61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
292 TGTTCCTCCCTTCAGACATATTTTGGCATCGTGTTCACAGATGTCACACGCTCTA 351
81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
352 TGGATATCTGAAATGACAGATGCTGTCAGTGAACAGCCATGAGCCCTGCTGTG 411
101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
412 AGGCTTGGCCAGTTTCCCAAGACTCCAGTGTGGATGAGGGGCGAGCTGATGGAAT 471
121 ValValLeuThrPAsnAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly 140
472 GTGCTTTTGTGGATGACACATCATACAAATTATATAGATGTGATGATTAAGATGCG 531
141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
532 TCCCTTGGCGCATGTGCAATTTCTCTAATGGAAGCTTCTTGTCACTGCGCTCATGT 591
161 GlyAspLeuThrValTTrpAspAspLysMetArgCysLysLeuHisSerGlyLysAlaHisAsp 180
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181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
652 CTTGGAATTAACCTGCTGCGATTTTCTTCAACAGCAAGTTTTCGATGAGGAACAAGTCTT 711
201 GlnPhePheAlaGlyLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrrIleValSer 220
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221 PheThrHisIleLeu----- 225
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225 ----- 225
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952 ACCAGTATGTCACAACTTGTGCTTTTGGACCACTAATACCTTTACTTCTGCTACTGTTCA 1011
226 ----- AlaArgArg 228
1012 ATGCAAAAACAGTGAACATCTGGCAATTGACCTGGAAACACTTTCGCCAAGCGGC 1071
229 ThrGlnHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValIleSerThrTrp 248
1072 ACAGAAATCATGCTGGAAGCAATTTTACCAAGATTGTCAGAGGAGATGTCCTCAACATGG 1131
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1132 CTTTGTGCACAGATTTTAAAGATCTTCTGCTGATTTTTCAGATGATTAACATTGATGCA 1191
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1192 AAAGAACTGTTGATCTTCAAAAAGAAAGTCTGCTGATGATTTGAAAAAT----- 1242
289 GlyLeuArgSerLysValLeuArgLysIleGluLeuLeuArgThrLysValLysSerLeu 308
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349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
1291 AAGAAAGTACAAATCCCATGACAAATCTGTTCTTCTTCAGGCGGATTAACCAAAAT 1350
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1351 AGGACTCTGAAATGCGCATCATATGATGCTGAGAGACACCAAAAG 1398

RESULT 3
AK011391
LOCUS
DEFINITION
MUS MUSCULUS 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610014F08 product:hypothetical SAM domain (Ser/ile alpha motif)/Modified RING finger domain/G-protein beta WD-40 repeats containing protein, full insert sequence.
AK011391
VERSION
AK011391.1 GI:12847483
KEYWORDS
HTC; CAP trapper.
SOURCE
MUS MUSCULUS (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
JOURNAL
METH. ENZYMOLOGY 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
20499374
PUBMED
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, O., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

[illegible]

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Qy	223	-----	228
Db	943	AAATCTGATCATATACATGATGATGGCCCTCAGAGTGTCTTACACACGCTGACTGATGAT	1002
Qy	229	ThrgluHis-----	231
Db	1003	ACCAAGTATGTTAGACCTTGCGCTTGACACCAACTCTCTTACTTGCTACTGCTTCA	1062
Qy	231	-----	231
Db	1063	ATGACAAGACAGTGAACATTTGGCAGTTTGACCTGAGAAACACTTGCACGAAGACATG	1122
Qy	232	-----GlnleuLysGlnPheThrGlnAspTrpSerGluGluValValSerThrTrrleu	249
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Qy	250	CysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGlyLys	269
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Qy	270	GluIleuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeuGly	289
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Qy	290	LeuArgSerLysValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeuSer	309
Db	1303	CTGGCAGCAAAAGCTCGAGAGATTCAGAGCTCAGGGCAAGATGATTCCTCTCT	1362
Qy	310	SerGlyIlePProAspGluPheIleCysProIleThrArgGluLeuMetLysAspProVal	329
Db	1363	TCCGGAATCCTTGACGAGGATTCATCTGCCAATTAACCAAGAACTCATAGAAGCCCCCTC	1422
Qy	330	IleAlaSerAspGlyTyrSerTyrGluLysGluAlaMetGluAsnTrpIleSerLysLys	349
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Qy	350	LysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsnArg	369
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AL553333			
LOCUS			
DEFINITION			
AL553333 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA			
clone CS001075H08 5-PRIME. mRNA sequence.			
ACCESSION			
AL553333			
VERSION			
AL553333.3 GI:45858102			
KEYWORDS			
EST.			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
Li, W.B., Gruber, C., Jesssee, J., and Polayars, D.			
Full-length cDNA libraries and normalization			
TITLE			
Unpublished (2001)			
JOURNAL			
COMMENT			
On Feb 15, 2001 this sequence version replaced gi:31275147.			
Contact: Genoscope			
Genoscope - Centre National de Sequenage			
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers			
end enriched, double-strand cDNA was digested with Not I and cloned			

into the NheI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1653.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdnat8=CS0D10750A04QP1cc=1653.r>.

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FEATURES
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                /clone="CSD01075YB08"
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                    sites of the pCMVSPORT 6 vector. Library was normalized."

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Alignment Scores:	
Pred. No.:	5, 48-112
Score:	1205, 00
Percent Similarity:	99.12%
Best Local Similarity:	98.23%
Query Match:	58.87%
DB:	1
US-10-077-111-13 (1-384) x AL553333 (1-889)	
	Length: 889
	Matches: 222
	Conservative: 2
	Mismatches: 1
	Indels: 1
	Gaps: 0

Qy	1	MetValIysLeuLIleHisThrLeuAlaAspHisSerIysAspAspValAsnGlyCysAlaPhe	20
Db	112	ATGGTGAACCTGATTACACATTACCTATCATGTGACGATGTCACACTGCTGGCCCTTC	171
Qy	21	SerPheSerLeuIleuAlaThrCysSerLeuAspIysThrIleArgLeuYrsSerLeuArg	40
Db	172	TCCCTTTCCCTCTGGCTACTTGCTGCTTGACAAACAAATTCGCTGACTCCCTTACGT	231
Qy	41	AspPheThrGluLeuProHisSerProLeuIysPheHisThrTrpAlaValHisCysCys	60
Db	232	GACTTTACTGAACCTGCCACATTTCTTCATTTGAAGTTTCACTTACTTACTGCTGCACTGCTGC	291
Qy	61	CysPheSerProSerGlyIysIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
Db	292	TGTTTTCTCCCTTCAGACATATTTTGGCATTCGTTCACACAGATGGATCACCATGTCCTTA	351
Qy	81	TrpAsnThrGluAsnGlyIleMetLeuAlaIleMetGluIleProSerGlySerProVal	100
Db	352	TGGAAATACGAAAAATGAGACAGATGCTGGCAGTACATGACACGCTTACGTGAGCAGCCCTGTG	411
Qy	101	ArgValCysGln-PheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr	120
Db	412	AGGGTTGGCAGTTTTTCCCGACCTCCACAGCGTTTGGCATCAGGGGACGCTGATGAC	471
Qy	120	IValValIleuThrPasnAlaGlnSerTrpIlyLeuTrpArgCysGlySerValIysAspGly	140
Db	472	TGTGTTTGTGGAATGACACATCTACAAATTAATATGATGTGTATGTATTAAGATGG	531
Qy	140	IysSerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	532	CTCCTTGGGGGAGTGGCCTTTTCTTCATATGGAAGCTTTCTTGTCACTGGCTCTCATG	591
Qy	160	SerGlyAspLeuThrValTrpAspAspIysMetArgCysLeuHisSerGlyIlyValAlaHisAs	180
Db	592	TGGTGATTTATCAGTGGATGATGAATAAATAGAGGTCTGATATGTAAAAAGACACATGA	651
Qy	180	PleuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLe	200
Db	652	TCTTGAATTAACCTGCTGGATTTTCTTTCACAGCAGATTTCTGATGGAGAACAAAGCTCT	711
Qy	200	uGlnPhePheAlaGluLeuAlaSerCysGlyGlnAspCysGlnValIlySileThrIleValIse	220
Db	712	TCAGTTTTTTCACATCGCATCATGTGGTMAAGATTGCGACATCAAAATTTGGATTTGTTTC	771

Qy	220	rphethrhisf1lelu	225
Db	772	TTTATCCCAATACCTTA	787
RESULT 5			
AL533510			
LOCUS	AL533510	941 bp	mRNA linear EST 24-MAR-2004
DEFINITION	AL533510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone		
	CGSDN004YV15 5-PRIME, mRNA sequence.		
ACCESSION	AL533510		
VERSION	AL533510.3	GI:45708442	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 941)		
AUTHORS	Lt.W.R., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 13, 2001 this sequence version replaced gi:31260591.		

Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segreg@genoscope.cns.fr Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers
enriched 1' double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRI sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1653. r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?seq=CS00DN004CE08OQP1&c=1653.r>.

FEATURES	Location/Qualifiers
source	1. .941

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/db_xref="taxon:9606"
/clone="CCSDN0041015"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_1b="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

Alignment Scores:

Pred. No.:	9.59e-112	Length:	941
Score:	1203.00	Matches:	220
Percent Similarity:	98.22%	Conservative:	1
Best Local Similarity:	97.78%	Mismatches:	4
Query Match:	58.77%	Indels:	0

US-10-077-111-13 (1-384) X AL533510 (1-941)

1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnGlyCysAlaPhe 20
167 ATGGGACACCGATTCCACACATTAGCGCATCATTGGTAGACGATGCCAATCGGTGSCCTTC 22

Qy 2 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuIyrSerLeuArg 40
Db 227 TCCCTTTCCCTCTGGCTACTGCTCCCTGGACAACAATTCGCCCTGTCCTTACGT 28

Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisLeuGlyGly 60
Db 287 GACCTTACTGAACCTGCACATCTCCATGAAAGTTTCAATCCATGTCTGCACACGCTGC 344

61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80

Db	347	TGTTTCTCCCTTCAGGACATATTTTGGCATCGTGTTCAACAGATGGTACACTGTCCTA	406
Oy	81	TRPAlenThGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
Db	407	TGGAAATACGAAAAATGGACAGATCGCTGGCAGTGATGGAAACAGCCTGATGGACCCCTGTG	466
Oy	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaIAspGlyThr	120
Db	467	AGGGTTTGGCAGTTTTCCTCCAGACTCCACGGTTTGGCATCAGGGAGCTGTATGGAACT	526
Oy	121	ValValLeuThrAsnAlaGlnSerTyrLeuTyrArgCysGlySerValIlyIAspGly	140
Db	527	GTGGTTTGTGGAAATGCCACAGCACAACMAATTATATAGATGTGTGATGTCTTAAGATGGC	586
Oy	141	SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys	160
Db	587	TCCTTGGCGCGMTGGCATTTTCTCTTAATGGAAAGCTTTTGTGCATCGCTCCTCATGT	646
Oy	161	GlyAspLeuThrValTTPAspAspIlyMetLeuArgCysLeuHisSerGlyIlyValAlaHisAsp	180
Db	647	GGGATTTTAAACGTGTGGATGATGATAAATGAGGGTCTGCATGTGTAAGAAAGACATGAT	706
Oy	181	LeuGlyIleThrCysCysAspPheSerGlnProValSerAspGlyGlnGlnGlyLeu	200
Db	707	CTTGGAAATTAAGCTGCTGGCATTTTCTTCAACAGCCAGTTTCTGATGGAGAAACAGGCTT	766
Oy	201	GlnPheArgLeuAlaSerCysGlyGlnAspCysGlnValIlyValIleTrrIleValSer	220
Db	767	CAGTTTTCCTGCAGCTGGCATGTGTGTGATGAGATTGCCAAGCAAAATTTGGATTGTTTCT	826
Oy	221	PheThrHisIleLeu 225	
Db	827	TTTACCATATCTTA 841	

RESULT	6
LOCUS	BMS43484
DEFINITION	BMS43484 1010 bp mRNA linear EST 20-FEB-2005 / RNA sequence.
ACCESSION	AF92519 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:572657
VERSION	BMS43484
KEYWORDS	BMS43484.1 GI:1873915 EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 1010)
AUTHORS
NIH-MGC <http://mgc.nhl.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph. D.

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5726572"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_1ib="NH MGC 124"
/note="Organ: brain; Vector: pCMV-SPORT6; site_1: EcoRV"

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QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
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Db 451 AGGGTTGGCAGTTTCCAGACTCCAGTCTTTGGCATTACGGGCGAGCTGATGAACT 510
QY 121 ValValLeuTrpAsnAlaGlnSerTyrTyrLeuTyrArgCysGlySerValLysAspGly 140
| | | | |
| | | | |
Db 511 GTGGTTTGGGAATGACAGCTGATACAAATATATGATGTGTGTATGTTAAAGATGGC 570
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
| | | | |
| | | | |
Db 571 TCTTGGCGGCAATGCAATTTCTCTTAATGAAGCTTTCTTGCACTGGCTCCTCAATGT 630
QY 161 GlyAspLeuThrValTyrAspAspLysMetArg-CysLeuHisSerGlnLysAlaHisAs 180
| | | | |
| | | | |
Db 631 GGGATTAAACAGTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 690
QY 180 PLeuGlyIleThrCysCysAsp--PheSerSerGln-ProValSerAsp-GlyGlyGln 198
| | | | |
| | | | |
Db 691 ATCTGGAAATACCGCTGGCGGATTTTCTTCTCAAGCAAGTCTCGATTTGGAGAACT 750
QY 199 GlyLeuGln--PhePheArgLeuAlaSer-CysGly-GlnAspCysGlnValLysIleTr 217
| | | | |
| | | | |
Db 751 GGTCTTAAAGTTTTCGAACTGGCATGCAATGTGTGTGCAAGATGGCCAAATTC 810
QY 217 PLeuAlaSer-PheThrHisIleLeuAlaArgArgThrGln 230
| | | | |
| | | | |
Db 811 GGATGGGTCCTTTTACCGATATCTTACCAAGGGGCAACAG 851
RESULT 8
BI821143 792 bp mRNA linear EST 04-OCT-2001
LOCUS 603035030F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176086 5'
DEFINITION mRNA sequence.
ACCESSION BI821143
VERSION BI821143.1 GI:15932693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 792)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgarbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHM11438 Row: 1 Column: 07
High quality sequence stop: 751.
Location/Qualifiers
1..792
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5176086"
/lab_host="DH10B"
/clone_id="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2,27e-94 Length: 792
Score: 1031.50 Matches: 212
Percent Similarity: 92.21% Conservative: 10
Best Local Similarity: 91.77% Mismatches: 10
Query Match: 50.39% Indels: 9
DB: 4 Gaps: 1
US-10-077-111-13 (1-384) x BI821143 (1-792)
QY 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysValAlaPhe 20
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Db 118 ATGTGAAATGATGATTCACACATTACCTGATCAAGTGAAGATTCATACCTATGCTGCTGC 177
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
| | | | |
| | | | |
Db 178 TCTTTTCCCTCTGGCTACTGCTC--CTGGACAAACAAATTCGCTGTACTGTTACGT 224
QY 41 AspPheThrGlnLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
| | | | |
| | | | |
Db 235 GACTTTTACGAACTGGACACTGCTCTCCATTGAAGATTTCATACCTATGCTGCTGC 294
QY 61 CysPheSerProSerGlnHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
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| | | | |
Db 295 TGTTTCCCTCCAGACACTAT-TTGGCATGCTGTTCAAAGATGTACCACTGTCTTA 353
QY 81 TrpAsnThrGlnAsnGlyGlnMetLeuAlaValMetGlnGlnProSerGlySerProVal 100
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Db 354 TGGAAATACGMAAATGAGACAGATGCTGGCAGTGAACAGCTATGTCACCCCTGTG 413
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlnValAlaAspGlyThr 120
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| | | | |
Db 414 AGGGTTGGCCAGTTTCCAGACTCCAGCTGATGTGTGCAATCAGGGGCACTGATGAACT 473
QY 121 ValValLeuTrpAsnAlaGlnSerTyrTyrLeuTyrArgCysGlySerValLysAspGly 140
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Db 474 GTGGTTTGGGAATGACAGCTGATACAAATTATATGATGTGTGTATGATGATGATGATG 533
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSer-Cy 160
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| | | | |
Db 534 TCTTGGCGGCAATGCAATTTCTCTTAATGAAGCTTTCTTGTCTGCTGCTCTCAATG 593
QY 160 sGlyAspLeuThrValTyrAspAspLysMetArgCysLeuHisSerGln-LysAlaHisA 180
| | | | |
| | | | |
Db 594 TGGTGAATTAACAGTGTGGGATGATAAATGAGGTGTGCAATGATGAATAAAGCTCATG 653
QY 180 sPLeuGlyIleThr-CysCysAspPheSerSerGlnProValSer-AspGlyGlnGlnG 199
| | | | |
| | | | |
Db 654 ATCTTGAATTAACCTTGTGCTGCGATTTTCTTTCACAGCAGTTTCTTGATGGAGAACAG 713
QY 199 YLeuGlnPhePheArg-LeuAlaSerCys-GlyGlnAspCysGlnValLys-IleTrpI 218
| | | | |
| | | | |
Db 714 TCTTCAAGTTTTCGCACTTGGCATGATGTGGGTCAGGATTTGGCATGCAACATTTGGAC 773
QY 218 eValSerPheThrHisIle 224
| | | | |
| | | | |
Db 774 TGTTACTTTTACCATAATT 792
RESULT 9
CN793033 728 bp mRNA linear EST 26-MAY-2004
LOCUS CN793033
DEFINITION 4127990 BARC 8BOV Bos taurus cDNA clone IMAGE_46102 5', mRNA
sequence.
ACCESSION CN793033
VERSION CN793033.1 GI:47689013
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

QY	1	metVallyslleuilehistrleuallaphisgilyaapavalaasrcyCyAlaIahe	20
Db	5	ATGGGAGGCGGATTC-ACGCTGGCTATACCGGTGATGACGTCAAGCTGCGCCCTTC	63
QY	21	SerPheSerleuAlaIaThrCysSerleuAspIystrIleargLeuTySerleuarg	40
Db	64	TGGCTGCGCTCTTGCCACCTGCTCTTTGGACAAAGACATCCGCTTACCTTAACT	123
QY	41	AspPheThrGluLeuProHisSerProleuLysPhehistrTyAlaValHisCyAs	60
Db	124	GACTTTCGTGAACCTCCGCTACTCCCGGTGAAGTTCACACCTAAGCTGCACAGCTGC	183
QY	61	CysPheSerProSerGIyHistrleuAlaSerCysSerThrAspGIyThrValleu	80
Db	184	TGTTTCTACCTCAGGACAGCTTTAGTCAITGCTCTGACAGACGGACCAAGCTCTG	243
QY	81	TrpAenthrgluAsnGIyGlmMetleuAlaValMetGluGlnProSerGIySerProAl	100
Db	244	TGGAGCTCGCACAGCGGACACACCTGACCGGTGGAGCAGCGGCTGGACCCCTGTG	303
QY	101	ArgValCysGlnPheSerProAspSerThrCysleuAlaSerGIyAlaAlaAspGIyThr	120
Db	304	CGCGCTGTGCTTTTCCCGAGCTCTGCTTACCTAAGGCTCAGGGGCTGCCAGTAGATCC	363
QY	121	ValValleuTrpAsnAlaGlnSerTyTrpLysleuTyArgCysGIySerValLysAspGIy	140
Db	364	ATTGCTTTGTGGAAITGCACAGACATCAAAACATATAGGTGTGTGATCAAGATAGC	423
QY	141	SerLeuAlaAlaIaCysAlaPheSerProAsnGIySerPhePheValThrGIySerSerCys	160
Db	424	TCATTGGTGGCGCTGTGCGCTTTTCTCCGATGAGGCGCTTTGTGTACGTGCTTCGGGCG	483
QY	161	GIyAspLeuThrValTrpAspAspLysMetArgCysLysHisSerGIyLysAlaHisAsp	180
Db	484	GGGGACTTGACAGTGTGGATGACAGATGAGTGTCTTACACAGCGAAGCGCAGCAT	543
QY	181	LeuGIyIleThrCysCysAspPheSerSerGlnProValSerAspGIyGluGlnIyLeu	200
Db	544	CTCGGATCACCCTGCTGCGAGCTTTTCTTCACAGCCTCTCTCGGGGAGAA---GGCCTC	600
QY	201	GlnPhePheArgLeuAlaSerCysGIyGlnAspCysGlnValLysIleTrpIleValSer	220
Db	601	CAGCTTACCACTTGGCGTCACTGTGTGTCAAGCATGTGAATCAAACTCTGGGCTTACT	660
QY	221	PheThrHisIleLeu 225	
Db	661	ATTACCCGCTCTTA 675	
RESULT 11			
LOCUS	BI107478	838 bp	mRNA
DEFINITION	60289315F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5039019 5',		linear
ACCESSION	BI107478		
KEYWORDS	EST.		
SOURCE	EST.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 838)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		

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Plate: L14M1107 row: m column: 04
High quality sequence stop: 830.
Location/Qualifiers
1. 838
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:5039019"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCW-SPOrt6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally; primer: oligo dT
library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

```

[illegible]

QY 234 LysGlnPheThrGluAspTrpSerGluValValSerThrTrpLeuGlyAla 251
 Db 654 ---AAAGACACACTAAAGTGGGCACTGGCCCTTCTCT---TGCGCTTGCT 701

RESULT 12

CK306752 839 bp mRNA linear EST 01-MAR-2004
 SB02035A1D03.f1 normalized Keck-Tagu Library SB02 Taeniopygia
 guttata cDNA clone SB02035A1D03.f1 5, mRNA sequence.

ACCESSION CK306752 GI:44816326
 VERSION CK306752.1 GI:44816326
 SOURCE Taeniopygia guttata
 ORGANISM Taeniopygia guttata
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
 Estrilidae; Taeniopygia.
 1 (bases 1 to 839)
 Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
 Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
 and Liu,L.
 The Songbird Neurogenomics Initiative: An Evolving Public Resource
 For Study of Genes, Brain, and Behavior
 Unpublished (2004)
 Contact: David F. Clayton
 University of Illinois
 B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
 Tel.: 217 244 3668
 Fax: 217 244 1648
 Email: dclayton@uiuc.edu
 Base Calling/Quality Scores: PHRED from Washington University
 Genome Center.
 Vector Trimming: Cross match from Washington University Genome
 Center PHRAP suite. Low quality bases (Phred score < 20) were
 trimmed from both ends of the sequence by an in-house script.
 This sequence is vector free and at least 200 bp in length. Funded
 by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative.'
 PCR primers
 FORWARD: TAAATGACGACTGACTAGG(T7)
 BACKWARD: ATTAACCTCCTCAAG(T7)
 Insert Length: 839 Std Error: 0.00
 Plate: SB02035A1 row: D column: 03
 Seq primer: TAAATGACGACTGACTAGG (T7)
 High quality sequence stop: 839.

FEATURES

Source location/Qualifiers

1..839

/organism="Taeniopygia guttata"
 /mol_type="mRNA"
 /db_xref="taxon:59729"
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 and adult (pooled)"
 /lab_host="DH10B"
 /clone_lib="normalized Keck-Tagu Library SB02"
 /note="Organ: brain; Vector: pBS II SK(+); Site 1:
 EcoRI(5' side of insert); Site 2: NotI (3' side of
 insert); The library was constructed and normalized as
 described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
 (1996), Genome Research 6(9): 791-806. An identifying tag
 was added at the 3' during cDNA synthesis:
 insertAAAAAAAAAAAAAAAAATGCA."

ORIGIN

Alignment Scores:

Pred. No.: 1.24e-81 Length: 839
 Score: 907.00 Matches: 161
 Percent Similarity: 84.00% Conservative: 28
 Best Local Similarity: 71.56% Mismatches: 36
 Query Match: 44.31% Gaps: 0
 DB: 7

US-10-077-111-13 (1-384) x CK306752 (1-839)

QY 1 MetVallysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysGlyAlaPhe 20
 Db 90 ATGGGACATTAAATTCACACTTATAGCAGATCATATGATGATTAATTAATCACTGCTTC 149

QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
 Db 150 TCATCTTGCTGCTTGGCTGACATGTTCTCTGGACAAACAAATTCGGCTATATCTTTGAGC 209

QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
 Db 210 AACTTCGCTGAGCTCCCTACTCTCCGCTTGAGGCTCAGCGTACCGCTGCACGCTGTC 269

QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
 Db 270 TGTCTTCTGCGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329

QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
 Db 330 TGGGACACCCGCATGGCGCGAGGCTGCGCTGCGAGCAGCCCGGCGCAGCCCTGTC 389

QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
 Db 390 AGGCTCTGCCCTCTCTCGCCGAGGCGCCTATCTCTTGGCAGGCGCAGCGATGGCAGC 449

QY 121 ValValLeuThrPheAlaGlnSerTyrIleLeuTyrArgCysGlySerValIleAspGly 140
 Db 450 GTGGTCTCTGGAACGTGCAGTCCATGATGAATCTTGGAGAAAGTTAAAGTGTGT 509

QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
 Db 510 TCTTTGATGGCTGTGTGATTTTCTCCCATGGAACCTTTGTGACATCATCAAGT 569

QY 161 GlyAspLeuThrValTTPAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
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QY 181 LeuGlyIleThrCysAspPheSerSerGlnProValSerAspGlyGluGlyLeu 200
 Db 630 CTGGCGTTACCTGTGTGATATTTCTTTCACATCCAGTATCTGATGAGTAAATGGAGTC 689

QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer 220
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QY 221 PheThrHisIleLeu 225
 Db 750 TTTCAGATTTCTTA 764

RESULT 13

CK792250 808 bp mRNA linear EST 25-FEB-2004
 LOCUS AGENCOURT.18674252 NIH_MGC_230 Mus musculus cDNA clone
 DEFINITION IMAGE:30845589 5', mRNA sequence.
 ACCESSION CK792250
 VERSION CK792250.1 GI:42804246
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@dbp-remail.nih.gov
 Tissue Procurement: Shioko Kimura/Atsushi Yamada, (NCI,CCR)
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)


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Db      2 GCTCCTGCAGACATATTTGGCATCGTGTTCACAGATGTAACCACTGCTCTATGGAAT 61
Qy      83 ThGluAnsglyGlnMetLeuAlaValMetGluGlnProSerGlySerProValArgVal 102
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RESULT 15
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DEFINITION 60304688F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187309 5',
mRNA sequence.
ACCESSION B1759505
VERSION   B1759505.1 GI:15751083
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LUM11467 row: 0 column: 22
            High quality sequence stop: 696.
            Location/Qualifiers
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                    /clone_lib="NIH MGC 116"
                    /note="Organ: pooled colon, kidney, stomach. Vector:
                    pCMV-SORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                    source anonymous pool of 3 colons, age 26 yo male, 49 yo
                    female, 71 yo male colon; 46 yo male kidney, and pool of 2
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stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	5,26e-79	Length:	696
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Percent Similarity:	100.00%	Conservative:	2
Best local Similarity:	98.77%	Mismatches:	0
Query Match:	42.99%	Indels:	0
DB:	4	Gaps:	0

US-10-077-111-13 (1-384) x B1759505 (1-696)

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Qy      123 LeuTPsmaAlaGlnSerTyrlsLeuTyraGcysGlySerValLysAspGlySerLeu 142
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Qy      223 HisIleLeu 225
Db      482 CATATCTTA 490
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Search completed: October 25, 2005, 04:07:23
Job time : 2834 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 03:22:31 ; Search time 715 Seconds

(without alignments)
4432.164 Million cell updates/sec

Title: US-10-077-111-13

Perfect score: 2047

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9772363 seqs, 4126298632 residues

Total number of hits satisfying chosen parameters: 19544726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1984	96.9	1553	14 US-10-077-111-3	Sequence 3, Appl
3	1984	96.9	1818	14 US-10-077-111-1	Sequence 1, Appl
4	1984	96.9	1996	21 US-10-357-930-23179	Sequence 23179, A
5	1984	96.9	1996	21 US-10-357-930-22046	Sequence 22046, A
6	1978	96.6	1773	17 US-10-287-218-40	Sequence 40, Appl
7	1978	96.6	1773	20 US-10-474-291-40	Sequence 40, Appl
8	1978	96.6	1817	18 US-10-104-047-1689	Sequence 1689, Ap
9	1978	96.6	1817	10 US-09-971-392-207	Sequence 207, App
10	1978	96.6	1844	16 US-10-037-270-768	Sequence 768, App
11	1978	96.6	1844	18 US-10-117-722-768	Sequence 768, App
12	1977	96.6	1821	22 US-10-956-157-5128	Sequence 5128, Ap
13	1958	95.7	1908	14 US-10-077-111-14	Sequence 14, Appl
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21	597	29.2	366	9 US-09-864-761-10657	Sequence 10657, A
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23	509	24.9	419	24 US-10-779-543-8962	Sequence 8962, Ap
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31	261.5	12.8	1631	22 US-10-764-420-2108	Sequence 2108, Ap
32	259.5	12.7	3082	9 US-09-764-853-29	Sequence 29, Appl
33	259	12.7	3082	19 US-10-451-207-18	Sequence 18, Appl
34	256.5	12.5	3166	19 US-10-451-207-13	Sequence 13, Appl
35	251	12.3	1137	18 US-10-369-493-31840	Sequence 31840, A
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40	242.5	11.8	1965	18 US-10-369-493-42753	Sequence 42753, A
41	242.5	11.8	3408	18 US-10-369-493-42733	Sequence 42733, A
42	236.5	11.6	3358	18 US-10-369-493-42532	Sequence 42532, A
43	234.5	11.5	2826	26 US-11-097-143-17132	Sequence 17132, A
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ALIGNMENTS

RESULT 1
US-10-077-111-12
; Sequence 12, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Todderud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, J11
; TITLE OP INVENTION: JBA
; FILE REFERENCE: 3053-411US2
; CURRENT APPLICATION NUMBER: US/10/077, 111
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294, 181
; PRIOR FILING DATE: 2001-05-29

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: Sequence 1, Application US/10077111
: Publication No. US20020187492A1
: GENERAL INFORMATION:
: APPLICANT: Toddlerud, C. Gordon
: APPLICANT: Finger, Joshua N.
: APPLICANT: Rillema, Jill
: TITLE OF INVENTION: TBA
: FILE REFERENCE: 3053-4114US2
: CURRENT APPLICATION NUMBER: US/10/077,111
: PRIORITY FILING DATE: 2002-02-15
: PRIOR APPLICATION NUMBER: 60/294,181
: PRIOR FILING DATE: 2001-05-29
: PRIOR APPLICATION NUMBER: 60/269,366
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1818
: TYPE: DNA
: ORGANISM: HUMAN
US-10-077-111-1
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Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
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Db 688 CTGGAAATTCCTGCTGGATTTTCTTCAAGCAGATTTCTGATGGAACAAGGCTTT 747
Qy 201 GluPhePheArgLeuAlaSerCySGLyGluAspCySGLuValLysIleTppIleValSer 220
Db 748 CAGTTTTTGCAGCTGGCATATGTCAGAGATTGCCAAGTCAAAATTTGGATTGTTCT 807
Qy 221 PheThrHisIleLeu----- 225
Db 808 TTTAACCATATCTTAGCTTTTGAATTAAATPATAAAGTACACTGAGTGGGCACTGTCT 867
Qy 225 ----- 225
Db 868 CCGTTCTGGCTTGCTGCTTTTCCCATGATGGCAGATGCTAGTCAAGGTCAGTGGAT 927
Qy 225 ----- 225
Db 928 AAGTCTGTCACTAGTATATGATACTAATACTGAGAATATACTTCACACATTGACTCAGCAC 987
Qy 225 ----- 225
Db 988 ACCAGATATGCACAACCTTGCTTTTGCACCTAATACCTTTTACTTGCTAGCTGTTCA 1047
Qy 226 -----AlaAspArg 228
Db 1048 ATGGAACAACAGTGAACATCTGGCAATTGACCTGGAAACACTTGGCCAAGAGCGC 1107
Qy 229 ThrGluHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValValSerThrTrp 248
Db 1108 ACGAACAATCACTGAGAACAAATTACCGAAGATTGGTCAAGAGAGATGCTCAACATGG 1167
Qy 249 LeuCySAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db 1168 CTTTGTGCACAAAGATTAAAGATCTTGTGGTATTTTCAAGATGAATTAACATTGATGA 1227
Qy 269 LysGluLeuLeuLeuLeuThrLysGluSerLeuAlaAspAspLeuLysIleGluSerLeu 288
Db 1228 AAGAACTGTTGAATCTTACAAAAGAAAGTCTGGCTGATGATTTGAAATTCCTTA 1287
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGluLeuArgThrLysValLysSerLeu 308
Db 1288 GGACTGGCTGTAAGTGTGAGGAAATTTGAAAGCTCAGAGACCAAGTTTAAATCCCTT 1347
Qy 309 SerSerGlyIleProAspGluPheIleCySProIleThrArgLysLeuMetLysAspPro 328
Db 1348 TCTTCAAGAAATTCCTGATGATTTATATATGTCAACTAAGAACTTATGAAGAATCCG 1407
Qy 329 ValIleAlaSerAspGlyTrpSerGlyGluLysGluAlaMetGluAsnTrpIleSerLys 348
Db 1408 GTATCCCATCAGATGGCTATTTCAATAGAAAGAAAGCAATGGAAATTTGGATCAGCAA 1467
Qy 349 LysLeuArgThrSerProMetThrAsnLeuValLeuProSerAlaValIleThrProAsn 368
Db 1468 AAGAAAGCTCAAGTCCCATGACAAATCTTGTCTTCAAGGAGTACTTACCACAAT 1527
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db 1528 AGGACTCTGAATAATGCCATCAATAGATGGCTGAGACACCAAAAG 1575

RESULT 4
US-10-357-930-23179
/, Sequence 23179, Application US/10357930

Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endesge, Wilson
APPLICANT: Nonahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION OF HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-0078CN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23179
LENGTH: 1996
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1_2_3_1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
LOCATION: 1995, 1996
OTHER INFORMATION: n = A, T, C or G
US-10-357-930-23179
Alignment Scores:
Pred. No.: 4,366-225 Length: 1996
Score: 1984.00 Matches: 363
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 21 Gaps: 1
US-10-077-111-13 (1-384) x US-10-357-930-23179 (1-1996)
Qy 1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCySAlaPhe 20
Db 16 ATGGTGAACCTGATTCACACATTAAGTATCATGTGAGAGATGTCAACTGCTGTGCTTC 75
Qy 21 SerPheSerLeuLeuAlaThrCySAspLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db 76 TCCCTTCCCTCTTGGCTATGCTCTTGGACMAAACAAATTCGCTGTAACCTGTTACGT 135
Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyraIaValHisCyS 60
Db 136 GACTTAACTGAACCTGCACATTTCTCATTTGAAGTTTCAATACCTATGCTGTCCACTGTC 195
Qy 61 CySAspSerProSerGlyHisIleLeuAlaSerCySAspThrAspGlyThrThrValLeu 80
Db 196 TGTCTTCCCTTCAGAGCATATTTTGGCATGCTGTTCAAACAGATGTAACACTGTCTTA 255
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 256 TGGAAATCTGAATAATGAGAGATGCTGGCAGATGAGAAACAGCTTATGTGCAAGCCCTGTG 315
Qy 101 ArgValCySGLuPheSerProAspSerThrCySLeuAlaSerGlyValAlaAspGlyThr 120
Db 316 AGGCTTGGCAGTTTTCCCAAGCTCCACAGCTGCTTTTGGCATTCAGAGGAGACTGATGAAC 375
Qy 121 ValValLeuTrpAsnAlaGlnSerTyrlLysLeuTyraArgCySGLySerValLysAspGly 140

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Db 376 GTGGTTTGGAGATGACAGTCACTATACAAATTATATAGATGTGTACTGTTAAAGATGC 435
Qy 141 SerLeuAlaAlaCysAlaPheSerProArgIySerPheValIThrGlySerSerCys 160
Db 436 TCCCTGGCGGCACTGTGATTTTCCCTTAATGAAAGCTTCTTGTCCACGTGGCTCTCATGT 495
Qy 161 GlyAspLeuThrValITrpAspAspLeuMetArgCysLeuHisSerGlyValAlaHisAsp 180
Db 496 GGTGATTTAAACAGTGTGGATGATTAATAAGAGTGTCTGATGATGAAAAGCACATGAT 555
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
Db 556 CTTCGAATTAACCTGCTCGATTTTCTTCCACAGCAGATTTCTGATGAGAAACAAGTCTT 615
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspGlnValValIleTrrPheValSer 220
Db 616 CAGTTTTCGACCTGGCATGTGTGTGAGATTCAGATTCAGCAAGTCAAAATTTGGATTGTTCT 675
Qy 221 PheThrHisIleLeu----- 225
Db 676 TTTAACCAATATCTTAGCTTTTGAATTAAATATATAAAAGTACACTGAGTGGCACTGTCT 735
Qy 225 ----- 225
Db 736 CCGTCTTGCGCTTGTGCTTTTCCCATGATGGGAGAGATGCTAGTCTCAGGCTCAGTGAT 795
Qy 225 ----- 225
Db 796 AAGTCTCATAGTATATGATACTAATACTGAGATATATTACTTACACATGACTCAGCAC 855
Qy 225 ----- 225
Db 856 ACCAGGATATGCACACTTGTGCTTTTGGACACTTAATACCTTTACTTGTCTACTGTTCA 915
Qy 226 ----- 226
Db 916 ATGCAAAACAGTGAACATCTGGCAATTGACCTGGAAACACTTTCGCAAGCAAGGCGC 975
Qy 229 ThrGlnHisGlnLeuValSerPheThrGlnAspTrrPheGlnValValSerThrTrr 248
Db 976 ACAGAAATCATGCTGAGCAATTTTACCAAGATTTGTCAGAGAGATGTCCTCAACATGG 1035
Qy 249 LeuCysAlaGlnAspLeuValGlyIlePheValMetAspHisIleAspGly 268
Db 1036 CTTTGTGCACAGATTTTAAAGATCTGTGTGATTTTCAAGATGAATTAACATGATGGA 1095
Qy 269 LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu 288
Db 1096 AAAGAACTGTTGATCTTACAAAAGAAAGTCTGCTGATGATTTGAAATTTGATCTCTA 1155
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
Db 1156 GGAATCGGTGTAAGTGTGAGGAAATTAAGAGCTCAGAGCAAGGTTAAATCCCTT 1215
Qy 309 SerSerGlyIleProAspGlnPheIleCysProIleThrArgGlnLeuMetLysAspPro 328
Db 1216 TCTTCAGGAATTCCTGATGAAATTTATATGTCAAATTAACATTAAGAACTTATAAAGATCCG 1275
Qy 329 ValIleAlaSerAspGlyTrrSerTrrGlnLysGlnAlaMetGlnAsnTrrPheSerLys 348
Db 1276 GTCAATCCCATCAGATGCTATTCATATCAAAAAGAAAGAAATGGAATTTGATCAGCAA 1335
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1336 AAGAAAGCTACAAATCCCATGACAAATCTTGTCTTCTTCCAGCGGTACTTACACAAAT 1395
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys 384
Db 1396 AGGACTCTGAATAATGGCCATCATATGATGCTGGAGACACACCAAAAG 1443

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: Sequence 29046, Application US/10357930
: Publication No. US2004025906A1
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Endege, Wilson
: APPLICANT: Monahan, John
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
: TITLE OF INVENTION: HUMAN PROSTATE CANCER
: FILE REFERENCE: MRI-007BCN
: CURRENT APPLICATION NUMBER: US/10/357,930
: CURRENT FILING DATE: 2003-02-04
: PRIOR APPLICATION NUMBER: 09/785,276
: PRIOR FILING DATE: 2003-02-16
: PRIOR APPLICATION NUMBER: 60/183,319
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/189,862
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: 60/207,454
: PRIOR FILING DATE: 2000-05-25
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: 60/219,007
: PRIOR FILING DATE: 2000-07-18
: PRIOR APPLICATION NUMBER: 60/255,281
: PRIOR FILING DATE: 2000-12-13
: NUMBER OF SEQ ID NOS: 62232
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 29046
: LENGTH: 1996
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 2, 3, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994,
: OTHER INFORMATION: n = A,T,C or G
US-10-357-930-29046

Alignment Scores:
Pred. No.: 4,36e-225 Length: 1996
Score: 1984.00 Matches: 383
Percent Similarity: 80.46% Conservative: 0
Best Local Similarity: 80.46% Mismatches: 1
Query Match: 96.92% Indels: 92
DB: 21 Gaps: 1

```

QY	121	ValValLeuTPASAlaGlnSerTyrLysLeuTyrAcCysGlySerValLysAspGly	14
Db	376	GTGGCTTTTCTGGAAATGCACAGTCATACAAATTATATAGATGTGGTGTAAAGATGGC	435
QY	141	SerLeuAlaAlaCysAlaPheSerProaengLysSerPhePheValThrGlySerSerCys	160
Db	436	TCTCTGGGGCGCATGTGCATTTTCTCCTAATGGAAGCTTTTGTCTCACTGGCTCCTCATGT	495
QY	161	GlyAspLeuThrValTTPraSpraSpraLysMetArgCysLeuHisSerGluLysAlaHisAsp	180
Db	486	GGTGATTTTACAGTGTGGATGATGATAAATGAGGTGTCTCATATGTGAAGAACATGTAT	555
QY	181	LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu	200
Db	556	CTTGGAATTAACCTGTGGCATTTTCTTCTTCCACAGCCAGTTTCTGATGGAGAACAAAGTCTTT	615
QY	201	GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleThrPileValSer	220
Db	616	CAGTTTTTTTGCATGGCATCATGTGTGATGATGCGCAAGTCAAATTTTGATGTGTTTGT	675
QY	221	PheThrHisIleLeu-----	225
Db	676	TTTACCCATATCTTACGTTTGATTAATAATATAAGTACACTGATGGGACGTGTCT	735
QY	225	-----	225
Db	736	CCTGTCTGGCTTGTGCTTTTTTCCCATGATGGGAGAGTCTGTCTCAGGGTCAATGGAT	795
QY	225	-----	225
Db	796	AAGTGTCTCATAGTATATGATACTAATACTGAGAAATATATCTTCCACACTGACTCAGCAC	855
QY	225	-----	225
Db	856	ACCAGGTATGTCACAACTGTGTCTTTTGACACCTAATACCCTTTTACTGTCTACTGTTC	915
QY	226	-----AlaArg	228
Db	916	ATGACAAAAACAGTAACATCTGGCAATTGACCTGGAAAACCTTTGCCAACAGACGGCCG	975
QY	229	ThrGlnHisGlnLeuLysGlnPheThrGlnAspTyrSerGlyGlnValValSerThrTyr	248
Db	976	ACAGAACTCAGCTGAGCAAGCAATTACCCGAAAGTGTGTCAAGAGAGATGTCTTCAACATGG	1033
QY	249	LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly	268
Db	1036	CTTTGTGCACAAAGATTAAAGATCTTGTGTGATTTTCAAGATGAATGAACATTGATGGA	1099
QY	269	LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu	288
Db	1096	AAAGAACTGTGAATCTTACAAAGAAAGCTGTGGCTGATGATTTGAAAATGTGATCTCTA	1155
QY	289	GlyLeuArgSerLysValLeuArgLysIleGlnGlnLeuArgThrLysValLysSerLeu	308
Db	1156	GGACTGCGTAAGTAAGTGCTGAGAAAATTTGAAGAGCTCAGAGCCAAAGGTAAATCTCTT	1211
QY	309	SerSerGlyIleProAspGlnPheIleCysProIleThrArgLysLeuMetLysAspPro	328
Db	1216	TCTTGAGGAATTCCTGATGAATTTATATGTCCAAATAACTAGAGAACTTATGAAGATCCG	1277
QY	329	ValIleAlaSerAspGlyTyrSerTyrGlnLysGlnAlaMetGlnAsnThrPileSerLys	348
Db	1276	GTCAATCGCATCGATGGCTATTCATATGTGAAGAGAAAGCAATGGAAAATTGGATCAGCAAA	1333
QY	349	LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProaen	368
Db	1336	AAGAAACGTAACAGTCCCATGTGCAAAATCTTGTCTTCTTCCAGCGGTACTTACCAACAAAT	1399
QY	369	ArgThrLysLysMetAlaIleAsnArgTTPLeuGlnThrHisGlnLys	384
Db	1396	AGGACTCTGAAAATGCGCATCATATGATGTGTGGAGACACACCCAAAAG	1443

US-10-287-218-40
Sequence 40 Application US/10287218
Publication No. US20030198975A1

GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
APPLICANT: BATRA, Sateev; BAUGHN, Mariah R.
APPLICANT: BECHA, Shanya D.; BOROWSKY, Mark L.
APPLICANT: BUFORD, Neil; DING, Li
APPLICANT: ELIOTT, Vicki S.; EMERLING, Brooke M.
APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
APPLICANT: GRIFFIN, Jennifer A.; HARFALLA, April J.A.
APPLICANT: HONCHERL, Cynthia D.; LAL, Preeti G.
APPLICANT: LEE, Soo Yeun; LU, Dyung Aina M.
APPLICANT: ARVITU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: REDDY, Roopa; SANJANMALA, Madhu, M.
APPLICANT: TANG, Y. Tom; WALIA, Nandinder K.
APPLICANT: WANG, Yu-mei, E.; WARREN, Bridget A.
APPLICANT: XU, Yuming; YANG, Junming
APPLICANT: YAO, Montigue G.; YUE, Henry
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH

FILE REFERENCE: PI-0417 USA
CURRENT APPLICATION NUMBER: US/10/267, 218
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: PCT/US02/11152
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/349,705
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/295,263
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/295,340
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/293,727
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/291,846
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/291,662
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/287,228
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/286,820
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/283,294
PRIOR FILING DATE: 2001-04-11

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 40
LENGTH: 1773
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030198975A1 7483131CB1

US-10-287-218-40

Alignment Scores:

Pred. No.:	Score:
1,88e-224	Length: 1773
1978.00	Matches: 382
Percent Similarity: 80.25%	Conservative: 0
Best Local Similarity: 96.25%	Mismatches: 2
Query Match: 96.63%	Indels: 92
DB: 17	Gaps: 1

US-10-077-111-13 (1-384) x US-10-287-218-40 (1-1773)

Cy 1 MetValysLeuiEhtstHrleuaIasphigIvAspaVaIaenCySryAlaphc 20
Db 60 ATGGAGAACTGATTCACACTTGCATGATCATGTCACTGAATGTCACCTGCTGCTC 119

21 SerpheSerLeuaualatrhCySerLeuaspLyStrIlleaGLEuTySerLeuarg 40

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QY 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
Db 1260 ICTTCAGAAATTCCTGATGAAATTTATATGTCCTACCAATACCTAGAGAACTTATGAAAGATCCG 1319
QY 329 ValIleLeuSerAspGlyTyrSerTyrGluGluGluValMetGluAsnTrpIleSerLys 348
Db 1320 GTCATGCGCATCAGATGGCTATTTCATATGAAAGAAAGAACAAATGGATCAGCAAA 1379
QY 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1380 AAGAAAGTCACGATGCCCATGACAAATCTTGTTCTTCCTTACGGGTACTTACACCAAT 1439
QY 369 ArgThrLeuLysMetAlaIleAsnArgTyrLeuGluIleThrHisGlnLys 384
Db 1440 AGGACTCTGAATAATGCCCATCATATGATGGCTGGAGACACCAAAAG 1487

RESULT 7
US-10-474-291-40
: Sequence 40: Application US/10474291
: Publication No US20040132042A1
: GENERAL INFORMATION:
: APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
: APPLICANT: BATRA, Sajeey; BAUGHN, Mariah R.
: APPLICANT: BECHA, Shanya D.; BOROWSKY, Mark L.
: APPLICANT: BURFORD, Neil; DING, Li
: APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
: APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
: APPLICANT: GRIFFIN, Jennifer A.; HARALILA, April J.A.
: APPLICANT: HONCHELL, Cynthia D.; LAU, Preeti G.
: APPLICANT: LEE, Soo Yeun; LU, Dyung Aina M.
: APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
: APPLICANT: REDDY, Roopa M.; SANJANMALA, Madhusudan M.
: APPLICANT: TANG, Y. Tom; CHAMLA, Narinder K.
: APPLICANT: WANG, Yu-Mei E.; WARREN, Bridget A.
: APPLICANT: XU, Yuming; YANG, Junming
: APPLICANT: YAO, Monique G.; YUE, Henry
: APPLICANT: ZEBARADJIAN, Yeganeh
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
: FILE REFERENCE: PI-0417 USN
: CURRENT APPLICATION NUMBER: US/10/474,291
: PRIOR FILING DATE: 2003-10-06
: PRIOR APPLICATION NUMBER: PCT/US02/11152
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: US 60/349,705
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: US 60/295,263
: PRIOR FILING DATE: 2001-06-01
: PRIOR APPLICATION NUMBER: US 60/295,340
: PRIOR FILING DATE: 2001-06-01
: PRIOR APPLICATION NUMBER: US 60/293,727
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: US 60/291,846
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: US 60/291,662
: PRIOR FILING DATE: 2001-05-16
: PRIOR APPLICATION NUMBER: US 60/287,228
: PRIOR FILING DATE: 2001-04-27
: PRIOR APPLICATION NUMBER: US 60/286,820
: PRIOR FILING DATE: 2001-04-26
: PRIOR APPLICATION NUMBER: US 60/283,294
: PRIOR FILING DATE: 2001-04-11
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PERL Program
: SEQ ID NO 40
: LENGTH: 1773
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: incycle ID No: 7483131CB1
: US-10-474-291-40

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Db 270 GACTTACTGACGACACATTCCTCATTTGAGTTTATACCTATGCTGCTCACTGCTGC 329
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 330 TGTTCCTCCCTTCAGACATATTTTGGCATTCGTGTTCAACAGATGTGACCATGCTCTTA 389
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 390 TGGAAATCTGAAAAATGACAGATGCTGCGACTGATGGAACAGCTTACTGAGCCCTGTG 449
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
Db 450 AGGGTTTGCCAGTTTCCCGAGACTCCACGTTGTCATCAGGGGACAGCTGATGAACT 509
Qy 121 ValValLeuThrPheAsnAlaGlnSerThrLysLeuThrArgCysGlySerValLysAspGly 140
Db 510 GTGGTTTGTGGAATGACAGCTCATACAAATTATATGATGCTGATGTTAAAGATGCG 569
Qy 141 SerLeuAlaAlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCys 160
Db 570 TCCTTGCGGAGTGTGATTTCTCTTAATGGAAGCTTCTTGCTGCTGCTCTCATGT 629
Qy 161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
Db 630 GGTGATTTAAACAGTGTGGATGATAAATAGAGTGTCTGCATGCTGAAAAAGCATGAT 689
Qy 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 690 CTGGAAATTCCTGCTCGATTTTCTTTCACAGCCAGTTTCTGATGAGAAACAAGTCTT 749
Qy 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer 220
Db 750 CAGTTTTCGACGTGCATATGTGTGAGATTGCCAAGTCAAAATTTGGATTGTTCT 809
Qy 221 PheThrHisIleLeu----- 225
Db 810 TTTAACCATATCTTAGTTTGAATTAAATATAAAAGTACAGTGGGCACTGTGCT 869
Qy 225 ----- 225
Db 870 CCTGTCTGCTGTGCTTTTCCCATGATGGGAGATGTACTCAGGGTCAGTGAT 929
Qy 225 ----- 225
Db 930 AAGTCTGTCAATGATATGATACTAATACTGAGAAATACTTCAACATGACTCAGCAC 989
Qy 225 ----- 225
Db 990 ACCAGATATGCACAACTTGTGCTTTTGCACTAATACCTTTTACTTGTGCTACTGTTCA 1049
Qy 226 -----AlaArgArg 228
Db 1050 ATGACAAACACAGTGAACATCTGCAATTGACCTGGAACACTTTCGCAAGAGAGC 1109
Qy 229 ThrGlnHisGlnLeuLysGlnPheThrGluAspTrpSerGluGluValValSerThrTrp 248
Db 1110 ACAGAAATACATGCTGAAGCAATTTTACGAAAGATTGGTCAGAGAGAGATGTCCTCAACATGG 1169
Qy 249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetCAsnAsnIleAspGly 268
Db 1170 CTTTGTTCACAAAGTTTAAAGATCTTGTGATTTTTCAGATGAAATGATGATGAGA 1229
Qy 269 LysGlnLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuValIleGluSerLeu 288
Db 1230 AAAGAACTGTGATCTTACAAAGAAAGTCTGCTGATGATTTGAAATTTGAATCTCTA 1289
Qy 289 GlyLeuArgSerLysValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeu 308
Db 1290 GGACTGCGTGAATGAAGTCTGAGAAATGAAAGCTCAGACACCAAGTTAAATCCCTT 1349
Qy 309 SerSerGlyIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328

Db 1350 TCTTCAGAAATCTCGATGATTAATTATGTCCATAACTAGAGAACTTATGAAAGATCCG 1409
Qy 329 ValIleAlaSerAspGlyTrpSerThrGluLysGluAlaMetGluAsnTrpIleSerLys 348
Db 1410 GTCATGCAATCAATGAGCTATTCATATGAAAGAACCAATGGAATTTGATTCAGCAA 1469
Qy 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1470 AAGAAAGTCAACAGTCCCATGACAAATCTTCTTCTTCAGGGTATCTTACCCAAAT 1529
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys 384
Db 1530 AGGACTCTGAATAATGGCCATCAATGATGCTGAGACACACCAAAG 1577
RESULT 9
US-09-971-392-207
Sequence 207, Application US/09971392
Publication No. US20030134283A1
GENERAL INFORMATION:
APPLICANT: Peterson, David P.
APPLICANT: Pearson, Cecelia I.
TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
FILE REFERENCE: PA-0029 US
CURRENT APPLICATION NUMBER: US/09/971,392
CURRENT FILING DATE: 2001-10-03
PRIORITY APPLICATION NUMBER: 60/237,652
PRIORITY FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PERL Program
SEQ ID NO 207
LENGTH: 1817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Template ID: 158923.9
US-09-971-392-207
Alignment Scores:
Pred. No.: 1,95e-224 Length: 1817
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 80.25% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 10 Gaps: 1
US-10-077-111-13 (1-384) x US-09-971-392-207 (1-1817)
Qy 1 MetValLysLeuIleHisThrIleAlaAspHisGlyAspAspValaLysCysValaPhe 20
Db 148 ATGTGAAACTGATTCACACATTAAGTATGATGATGATGATGATGATGATGATGATGATG 207
Qy 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTrpSerLeuArg 40
Db 208 TCCTTTTCCTCTTGTGCTACTTGTCTCTTGGACAAAACAATTGCTGCTGCTGCTGCTGCT 267
Qy 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyralaValHisCysCys 60
Db 268 GACTTACTGAACTGCACAAATTCATGATGAAATTTCAATGATGATGATGATGATGATGATG 327
Qy 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db 328 TGTTCCTCCCTTCAGACATATTTTGGCATTCGTGTTCAACAGATGTGATGATGATGATG 387
Qy 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 388 TGGAAATCTGAAAAATGACAGATGCTGCGACTGATGGAACAGCTTACTGAGCCCTGTG 447
Qy 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr 120
Db 448 AGGGTTTGCCAGTTTCCCGAGACTCCACGTTGTCATCAGGGGACAGCTGATGAACT 507

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QY 121 ValValLeuTriPAsnA1aGInSerTyLyLeuTyTrArgCysGlySerValLyAspGly 140
DB 508 GTGGTTTGTGGAATGCACAGTCATCAAAATTATATGATGTGTGTTAAAGATGGC 567
QY 141 SerLeuAlaAlaCysAlaPheSerProAenGlySerPheHeValThrGlySerSerCys 160
DB 568 TCCCTGGCGGACATGTCATTTCTCCAAAGAGAGCTTCTTGTCTCAGCTGGCTCCATGCT 627
QY 161 GlyAspLeuThrValTriPAsnA1aGInSerTyLyLeuTyTrArgCysGlySerValLyAsp 180
DB 628 GGTGATTTAAACATGTCGGATGATAAATAGGTGTCTGATAGTGAAGAAAGACATGAT 687
QY 181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyGlnGlnGlyLeu 200
DB 688 CTGGAAATTACCTGCTGCGATTTTCTTCTCAGCCAGATTCTGATGGAGAACAGGCTCT 747
QY 201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLyIleThrPleValSer 220
DB 748 CAGTTTTTTCGACGTCATCATGTGTGTCAGGATTTGCCAAATTTGGATTTGTTCT 807
QY 221 PheThrHisIleLeu----- 225
DB 808 TTTAACCATATCTTAGGTTTGAATTAATAATATAAAAGTACAGTGGGACAGTGTCT 867
QY 225 ----- 225
DB 868 CCTGTTCTGGCTTGTGCTTTTTCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 927
QY 225 ----- 225
DB 928 AAGTCTGTCTAGTATATGATACTAATACTGAGAAATTACTTCAACATTGACTCAGCAC 987
QY 225 ----- 225
DB 988 ACCAGGATGTCAACACTGTGCTTTTGCACCTAATACCTTTACTTGTCTAGCTGTTCA 1047
QY 226 ----- 226
DB 1048 ATGAGCAAAACAGTGAACATCTGCAATTTGACCTGGAAACACTTGGCCAAAGAGAGC 1107
QY 229 ThrGluHisGlnLeuLySerGlnPheThrGluAspTrpSerGlnGluValValSerThrTrp 248
DB 1108 ACGAAATCATGCTGAGCAATTTACCGAAGATTGGTCAAGAGGAGATGTCTCAACACTGG 1167
QY 249 LeuCysAlaGlnAspLeuLyAspLeuValGlyIlePheLySerMetAsnAsnIleAspGly 268
DB 1168 CTTGTGTGCACAAATTTAAAGATCTTGTGTGATTTTCAAGATGAATTAACATTGATGCA 1227
QY 269 LySGlnLeuLeuAsnLeuThrLySGlnSerLeuAlaAspAspLeuLyIleGlnSerLeu 288
DB 1228 AAAAGAACTGTTGAATCTTCAAAAAGAAAGCTGCGTGTGATTTGAAAATTTGAATCTCTA 1287
QY 289 GlyLeuAspSerLyValLeuArgLyIleGlnGlnLeuArgThrLySerValLySerLeu 308
DB 1288 GGACTGTGATGAAGGCTGAGGAAATGAAAGAGCTCAGACCAAGGTTAAATCCCTT 1347
QY 309 SerSerGlyIleProAspGlnPheIleCysProIleThrArgGlnLeuMetLyAspPro 328
DB 1348 TCTTTCAGGAATTTCTGATGATTTATATATGTCAAATACTAGAGACTATGAAAGATCCG 1407
QY 329 ValIleAlaSerAspGlyTyTrSerTyGlnLyGlnAlaMetGlnLeuThrPleSerLyS 348
DB 1408 GTTCATGCAATCAATGCTATTCATATGAAAGAAAGCAATGAAATAATTTGATCAGAGAA 1467
QY 349 LySLeuAspThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
DB 1468 AAGAAACGTAAGAGTCCCATGACAAATCTTGTCTTCTTCAAGGACTACTTAACCAAAAT 1527
QY 369 ArgThrLeuLySerMetAlaIleAsnArgTrpLeuGlnThrHisGlnLyS 384
DB 1528 AGGACTCTGAATAATGGCCATCAATAGATGCTGAGAGCAACACCAAAAG 1575

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RESULT 10

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US-10-037-270-768
; Sequence 768, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Aseudi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Weinman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 768
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-037-270-768
Alignment Scores:
Pred. No.: 2e-224 Length: 1844
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best Local Similarity: 96.63% Mismatches: 2
Query Match: 96.63% Indels: 92
DB: 16 Gaps: 1
US-10-077-111-13 (1-384) x US-10-037-270-768 (1-1844)
QY 1 MetValLyLeuIleHisThrLeuAlaAspHisGlyAspAspValAunCysCysAlaPhe 20
DB 164 ATGGTAACCTGATTTACATCACTTACGTCATCATGTCGACGATGTCAATGCTGTGCTTC 223
QY 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLySThrIleArgLyCysTrpSerLeuArg 40
DB 224 TCTTTTCCCTCTTGTGCTAGTCTGCTCTTGGACAAAACAATTCGCTGACTGTTAGCT 283
QY 41 AspPheThrGlnLeuProHisSerProLeuLySProLeuHisThrTyTrAlaValHisCysCys 60
DB 284 GACTTACTGMACTGCGACATTTCTCATTTGAAGTTTCATTAACCTATGCTGTCCACTGCTGC 343
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
DB 344 TGTCTTCCCTCCCTTCAGAGACATATTTTGGCATGCTGTTCACACAGATGTACCACTGCTCT 403
QY 81 TrpAsnThrGluAsnGlyGlnMetLeuAlaValMetGlnGlnProSerGlySerProVal 100
DB 404 TGGAAATATCGAAAAATGACAGATGTGCGCAGATGTGAACAGCTGAGTGGACGCCCTGTG 463
QY 101 ArgValCysGlnPheSerProAspSerThrCysGlnAlaSerGlyValAlaAspGlyThr 120

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Db      464 AGGGTTTCCAGCTTTCCAGACTCCAGCTGTTGGCATCAGGGGAGCTGATGAACT 523
Qy      121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrTrgCysGlySerValLysAspGly 140
Db      524 GTGGTTTGGGAATGACAGTCAATACAAATTATATGATGTGTACTGTTAAAGATGGC 583
Qy      141 SerLeuAlaIaCysAlaPheSerProAsnGlySerPheValTrpGlySerSerCys 160
Db      584 TCCTTGGGGCAGTGTGATTTTCTCCTAATGGAAGCTTTCTTGTCACCTGGCTCTCACT 643
Qy      161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysAlaHisAsp 180
Db      644 GTGATTTAACAGTGTGGATGATTAATAATGAGTGTCTGCATAGTGAAGAAAGCAGATGAT 703
Qy      181 LeuGlyIleThrCysCysAspPheSerSerGlnProValSerAspGlyLysGlnGlyLeu 200
Db      704 CTGGGAATTACCTGCGCGAATTTTCTTTCACAGCAATTTCTGATGGAAGAAAGGCTCTT 763
Qy      201 GlnPhePheArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSer 220
Db      764 CAGTTTTTGGACTGGCATGTGTGTGTCAGAGATTGCCAAGCAAAATTGGATTGTTTCT 823
Qy      221 PheThrHisIleLeu----- 225
Db      824 TTTAACCATATCTTAGGTTTGAATTAATAATATAAGTACACTGAGTGGGCACTGTGCT 883
Qy      225 ----- 225
Db      884 CTTGTTCTGCGCTTGCTGCTTTTCCCATGATGGGAGATGCTAGTCTCAGGCTCAGTGAT 943
Qy      225 ----- 225
Db      944 AAGTCTGTCAATGATATGATACTAATACTGAGAATATACTTCAACATTGACTCAGAC 1003
Qy      225 ----- 225
Db      1004 ACCAGGATATGCACACACTTGCTTTGGACACTAATACCTTTACTTGCTACTGTTCA 1063
Qy      226 -----AlaArgArg 228
Db      1064 ATGACAAACAGTGAACATCTGCGCAATTGACCTGGAACACTTGGCCAGAGCAAGAGC 1123
Qy      229 ThrGlnHisGlnLeuLysGlnPheThrGlnAspTrpSerGlnGlnValIleValSerThrTrp 248
Db      1124 ACAGAAATCACTGCAAGCAATTTACCGAAGATTGTGTCAAGAGGAGATGTCTCAACATGG 1183
Qy      249 LeuCysAlaGlnAspLeuLysAspLeuValGlyIlePheLysMetAsnAsnIleAspGly 268
Db      1184 CTTTGTGCACAAAGATTAAAGATCTTGTGTGATTTTTCAGATGAATTAACATTGATGGA 1243
Qy      269 LysGlnLeuLeuAsnLeuThrLysGlnSerLeuAlaAspAspLeuLysIleGlnSerLeu 288
Db      1244 AAAGAACTGTTGAATCTTACAAAGAAAGCTGTGCTGATGATTTGAAATTTGAATCTCTA 1303
Qy      289 GlyLeuTrpSerLysValLysArgLysIleGlnGlnLeuArgThrLysValLysSerLeu 308
Db      1304 GGACTGCTGTAATAAGTCTGAGGAAATTTGAAGCTCAGAGACCAAGTTAAATCCCTT 1363
Qy      309 SerSerGlyIleProAspGlnPheIleCysProIleThrArgGlnLeuMetLysAspPro 328
Db      1364 TCTTCAGGAATCTCGATGAATTTATATGTCCAATTAAGTAAGAACTTATGAAGATCCG 1423
Qy      329 ValIleLeuSerAspGlyTyrSerTyrGlnLysGlnLysMetGlnAsnTrpIleSerLys 348
Db      1424 GTCAATCCATCAGATGGCTATTCATATGAAGAAAGAAAGCAATTTGATGAGCAAA 1483
Qy      349 LysLysArgTrpSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db      1484 AAGAAACATCAAGATCCCATACCAATTTCTTCTTCTTCAAGCGTACTTACACCAAT 1543
Qy      369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGlnThrHisGlnLys 384
Db      1544 AGGACTCTGAATAATGGCCATATGATGCTGAGAGACACCAAAAG 1591

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RESULT 11
US-10-117-722-768
; Sequence 768, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Dumanac, Radjoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 768
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1594)
US-10-117-722-768

Alignment Scores:
Pred. No.: 2e-224 Length: 1844
Score: 1978.00 Matches: 382
Percent Similarity: 80.25% Conservative: 0
Best local Similarity: 96.63% Mismatches: 2
Query Match: 18 Gaps: 1

US-10-077-111-13 (1-384) x US-10-117-722-768 (1-1844)
Qy      1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20
Db      164 ATGGTGAACGATTCACACATTTAGCTGATCATGTACATGTCACTGCTGCTTC 223
Qy      21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40
Db      224 TCCTTTCCCTCTGGCTACTGCTCTCTTGGACAAACAAATTCGCTGTAAGTCTTAAGT 283
Qy      41 AspPheThrGlnLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
Db      284 GACTTTACTGAACGACCAATTCCTCAATTGAAGTTTCAATGATGCTGTCCACGCTGC 343
Qy      61 CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu 80
Db      344 TGTTTCCCTTCAGGACATATTTTGGCATTCGTTTCAACAGATGTATCCACTGTCTTA 403
Qy      81 TrpAsnThrGlnAsnGlyGlnMetLeuAlaValMetGlnGlnProSerGlySerProVal 100
Db      404 TGGAACTGTAAGAAATGACAGATGCTGCAAGTGAACAGCTTACTGACAGCCCTGTG 463
Qy      101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaIleAspGlyThr 120
Db      464 AGGGTTTGCAGATTTTCCAGACTCCACAGTGTGTGCAATCAGGGGCAAGCTGATGAAC 523
Qy      121 ValValLeuTrpAsnAlaGlnSerTyrLysLeuTyrTrgCysGlySerValLysAspGly 140
Db      524 GTGGTTTGGGAATGACAGTCAATACAAATTATATGATGTGTACTGTTAAAGATGGC 583
Qy      141 SerLeuAlaIaCysAlaPheSerProAsnGlySerPheValTrpGlySerSerCys 160

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Db 584 TCCTTGCGGCATGTCATTTCTCCTAATGAAAGCTTTTTCAGTGGCTCCCTCATG 643
QY 161 G|YAsp|leu|thr|val|trp|asp|arg|leu|his|ser|gly|val|his|asp 180
Db 644 GGTGATTTTAACTGAGTGGAGTGAATAAGGTGCTGATGTGAAAAAGCACATGAT 703
QY 181 LeuG|Y|le|Thr|Cys|Cys|asp|phe|ser|ser|Gln|pro|val|ser|asp|Gly|Gln|Gly|Leu 200
Db 704 CTGGAAATTACCTGCTGCATTTTCTTCTTCAAGCAGATTTCTGATGGAGAAACAAGTCTT 763
QY 201 Gln|phe|phe|arg|leu|ala|ser|Cys|Gly|Gln|asp|Cys|Gln|Val|yl|et|p|l|le|val|Ser 220
Db 764 CAGTTTTTTTGACGTGCATCATGTGTCAGAGATTGCCAAGTCAAAATTTGGATTGTTCT 823
QY 221 Phe|Thr|His|leu|----- 225
Db 824 TTTTACCATATCTTATAGTTTGAATTAAATATATAAAGTACACTGAGTGGCAGCTGTCT 883
QY 225 ----- 225
Db 884 CCGTTCTGCGCTTGCTTTTCCCATGATGGCAGATGTCAGTCTCAGGGTCAGTGGAT 943
QY 225 ----- 225
Db 944 AAGCTGTCTAGTATATGATGACTAATATCTAGAGATATACCTTACACATTTGACTCAGAC 1003
QY 225 ----- 225
Db 1004 ACCAGGATGTCACAACTTGTGCTTTGGACCTAATACCTTTTACTTGCTACTGCTCA 1063
QY 226 -----Ala|arg|Arg 228
Db 1064 ATGGAACAAACAGTGAACATCTGGCAATTTGACCTGGAAACACTTTGCCAAGCAGAGAGC 1123
QY 229 Thr|Gln|His|Gln|leu|ys|Gln|phe|Thr|Gln|asp|Trp|Ser|Gly|Val|Val|Ser|Thr|Trp 248
Db 1124 ACAGAACTATCAGTGTGAAGCAATTTTACGAGATTTGGTCAGAGAGGATGTCCTCAACATGG 1183
QY 249 Leu|Cys|Ala|Gln|Asp|leu|ys|Asp|leu|Val|Gly|le|phe|ys|Met|Asn|Asn|le|asp|Gly 268
Db 1184 CTTTGTGCACAACTTTTAAAGATCTTGTGGTATTTTCAAGATGATTAACATTTGATGGA 1243
QY 269 Lys|Gln|leu|leu|Asn|leu|Thr|Lys|Gln|Ser|Leu|Ala|Asp|Asp|leu|ys|le|Gln|Ser|Leu 288
Db 1244 AAGAACTGTTGAATCTTACAAAAGAAAGTCTGGCTGATGATTTGAAAATTTGAATCTCTA 1303
QY 289 Gly|Leu|Asp|Ser|Lys|Val|Leu|arg|Lys|le|Gln|Gln|leu|arg|Thr|Lys|Val|Lys|Ser|Leu 308
Db 1304 GGACTGCGTAGTAAGTGTGAGGAAAAATTGAAGAGCTCAGACCAAGGTTTAAATCCCTT 1363
QY 309 Ser|Ser|Gly|le|Pro|Asp|Gln|phe|le|Cys|Pro|le|Thr|arg|Gln|leu|Met|Lys|Asp|Pro 328
Db 1364 TCTTTCAGGAATTTCTGATGAATTTATATGTCCAATATAGAGAACTTATGAAAGATCCG 1423
QY 329 Val|le|le|Asp|Ser|asp|Gly|Trp|Ser|Trp|Gln|Lys|Gln|Ala|Met|Gln|Met|Trp|le|Ser|Lys 348
Db 1424 GTCATGCGCATCAATGGCTATTCATATGAAAGAAAGAAAGCAATGAAATTTGATCAGAGAA 1483
QY 349 Lys|Lys|Arg|Thr|Ser|Pro|Met|Thr|Asn|Leu|Val|Leu|Pro|Ser|Ala|Val|Leu|Trp|Pro|Asn 368
Db 1484 AAGAAACGTAACAAGTCCCATGACAAATCTTGTCTTCTTCAAGGGGACTTATACCAAAAT 1543
QY 369 Arg|Thr|leu|ys|Met|Ala|le|Asn|arg|Trp|Leu|Gln|Thr|His|Gln|Lys 384
Db 1544 AGGACTCTGAATAATGGCCATCAATAGTGGCTGAGACACACCAAAAG 1591
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RESULT 12
US-10-956-157-5128

; Sequence 5128, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

```
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTIASES;  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5128  
; LENGTH: 1821  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-5128  
  
Alignment Scores:  
Pred. No.: 2,578-224 Length: 1821  
Score: 1977.00 Matches: 382  
Percent Similarity: 80.25% Conservative: 0  
Best Local Similarity: 80.25% Mismatches: 2  
Query Match: 96.58% Indels: 92  
DB: Gaps: 1  
  
US-10-077-111-13 (1-384) x US-10-956-157-5128 (1-1821)  
  
QY 1 Met|Val|Lys|leu|le|His|Thr|leu|Ala|Asp|His|Gly|Asp|Arg|Val|Asn|Cys|Cys|Ala|Phe 20  
Db 159 ATGATGAACCTGATTCACACATTAGCTGATCATGTGACAGATGTCAACTGCTGCTTAC 218  
QY 21 Ser|Phe|Ser|leu|leu|Ala|Thr|Cys|Ser|leu|Asp|Lys|Thr|le|Arg|leu|Trp|Ser|leu|Arg 40  
Db 219 TCCTTTCCCTCTTGCTGCTAGCTGCTCTTGGAACAAACATTTGCTGATCTGTTACGT 278  
QY 41 Asp|Phe|Thr|Gln|leu|Pro|His|Ser|Pro|Leu|Lys|Phe|His|Thr|Trp|Ala|Val|His|Cys|Cys 60  
Db 279 GACTTTACTGAACTGACACATTTCTCATTTGAACTTTCATACCTATCTGTCCCTGCTGC 338  
QY 61 Cys|Phe|Ser|Pro|Ser|Gly|His|le|leu|Ala|Ser|Cys|Ser|Thr|Asp|Gly|Thr|Val|Leu 80  
Db 339 TGTTCCTCCCTTCAGAGACATATTTGGCATCGTTCAACAGATGTCACACTGCTGCTTA 398  
QY 81 Trp|Asn|Thr|Gln|Asn|Gln|Gln|Met|leu|Ala|Val|Met|Gln|Gln|Pro|Ser|Gly|Ser|Pro|Val 100  
Db 399 TGGAAATACGAAATATGACAGATGCTGGCAGTGATGAAACACGCTGTGTCAGCCCTGTC 458  
QY 101 Arg|Val|Cys|Gln|Phe|Ser|Pro|Asp|Ser|Thr|Cys|leu|Ala|Ser|Gly|Ala|Asp|Gly|Thr 120  
Db 459 AGCGTTTGCAGATTTTCCCAAGCTCCACAGCTGTTTGCCATCAGGGGCAGCTGATGGAAGCT 518  
QY 121 Val|Val|leu|Trp|Asn|Ala|Gln|Ser|Trp|Lys|Leu|Trp|Arg|Cys|Gly|Ser|Val|Lys|Asp|Gly 140  
Db 519 GTGGTTTGTGGAAATGACAGATCATATTAATAATATATAGATGTGTGATGTTAAAGATGCG 578  
QY 141 Ser|leu|Ala|Ala|Cys|Ala|Phe|Ser|Pro|Asn|Gln|Lys|Pro|Phe|Val|Thr|Gly|Ser|Ser|Cys 160  
Db 579 TCCTTTGCGGCATGTCATTTTCTCCTAATGGAAGCTTCTTGTGTCAGCTGCTCTTCATATG 638  
QY 161 Gly|Asp|leu|Thr|Val|trp|Asp|Arg|Lys|Met|Cys|Arg|leu|His|Asp|Gln|Lys|Ala|His|Asp 180  
Db 639 GGTGATTTTAACTGAGTGGAGTGAATAAATGAGGTGTCGCCCATATGTAATAAAGACACATGAT 698  
QY 181 Leu|Gly|le|Thr|Cys|Cys|asp|phe|Ser|Ser|Gln|pro|val|ser|asp|Gly|Gln|Gly|Leu 200  
Db 699 CTGGAAATTACCGTGCATGATTTTCTTCAAGCCAGTTTTCATGATGGAACAAAGAGTCTTT 758  
QY 201 Gln|phe|phe|arg|leu|Ala|ser|Cys|Gly|Gln|asp|Cys|Gln|Val|Lys|le|Trp|Lys|Val|Ser 220  
Db 759 CAGTTTTTTTGACGTGCATCATGTGTCAGAGATTGCCAAGTCAAAATTTGGATTGTTCT 818  
QY 221 Phe|Thr|His|leu|----- 225  
Db 819 TTTACCATATATCTTATAGCTTTTGAATTAATAATATAAAGTACACTGAGTGGCAGCTGTCT 878  
QY 225 ----- 225
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Db 879 CTTGTTCTGGCTTGTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 938
QY 225 ----- 225
Db 939 AAGTCTGTCATAGTATATGATTAATACTGAGAAATTAATTCTTCAACATTGACTCAGCAC 998
QY 225 ----- 225
Db 999 ACCAGGATATGCACAACTTGCTTTTGCACTTAATACCTTTTACTTGCTACTGCTTCA 1058
QY 226 ----- 226
Db 1059 ATGACAAACAGTGAACATCTGCAATTTGACCTGGAACACTTTCCTCAAGCGC 1118
QY 229 ThcGluHtGlnLeuYsgInPheThcGluAspTrpSerGluGluValValSerThcTrp 248
Db 1119 ACAGAAATCATCGCTGAAGCAATTTTACCAAGATTGGTCAAGAGAGATGTCTCAACATGG 1178
QY 249 LeuCYsAlaGlnAspLeuLYsAspLeuValGlyIlePheLYsMetAsnAlaAspGly 268
Db 1179 CTTTGTGCACAGATTTTAAAGATCTTGTTGTAATTTTCAAGATGAATACATTGATGGA 1238
QY 269 LysGluLeuLeuAsnLeuThrLYsGluSerLeuAlaAspAspLeuLYsIleGluSerLeu 288
Db 1239 AAGAACTGTTGAATCTTACAAAGAAAGCTGCTGATGATTTGAAATTTGAATCTCTA 1298
QY 289 GlyLeuArgSerLYsValLeuArgLYsIleGluGluLeuArgThrLYsValLYsSerLeu 308
Db 1299 GGACTGCTAGTAAAGCTGAGAGAAATTTGAAGCTCAGAGCAAGTTAAATCCCTT 1358
QY 309 SerSerGlyIleProAspGluPheIleCYsProIleThrArgGluLeuMetLYsAspPro 328
Db 1359 TCTTCAGGAATCTCTGATGATTTTATATGTCATTAAGTAAAGATTTTAAAGATCCG 1418
QY 329 ValIleAlaSerAspGlyLYsSerLYsGluGluAlaMetGluAsnTrpIleSerLYs 348
Db 1419 GTCATCCCATCAGATGCTTATTCATATGAAAGAAAGCAATGAAATTTGGATCAGCAA 1478
QY 349 LysLYsArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db 1479 AAGAAAGCTAACAGTCCCATGACAAATCTTGTTCTTCTCAGCGTACTTACACCAAT 1538
QY 369 ArgThrLeuLYsMetAlaIleAsnArgTrpLeuGluThrHisGlnLYs 384
Db 1539 AGGACTCTGAAAAATGCCCATCAATAGATGCTGAGACACACCAAG 1586

RESULT 13
US-10-077-111-14
; Sequence 14, Application US/10077111
; Publication No. US20020187492A1
; GENERAL INFORMATION:
; APPLICANT: Toddlerud, C. Gordon
; APPLICANT: Finger, Joshua N.
; APPLICANT: Rillema, Jill
; TITLE OF INVENTION: TBA
; FILE REFERENCE: 3053-411AUS2
; CURRENT APPLICATION NUMBER: US/10/077,111
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/294,181
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/269,366
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: RET 16.3 splice variant
US-10-077-111-14

Pred. No.: 5,1e-222 Length: 1908
Score: 1958.00 Matches: 382
Percent Similarity: 76.29% Conservative: 1
Best Local Similarity: 76.10% Mismatches: 1
Query Match: 95.65% Indels: 118
Gaps: 2
US-10-077-111-13 (1-384) x US-10-077-111-14 (1-1908)

QY 1 MetValLYsLeuIleHisThrLeuAlaAspHisGlyAspAspValIleAspCYsAlaPhe 20
Db 136 ATGCTGAACCTGATTCACACATTAAGCTGATCATGTCACATGCTCACTGCTTTC 195
QY 21 SerPheSerLeuLeuAlaThrCYsSerLeuAspLYsThrIleArgLeuLYsSerLeuArg 40
Db 196 TCTTTTCCCTCTTGCTGCTACTGCTCTTGGACAAACAAATTCGCTGACTGCTTACGT 255
QY 41 AspPheThrGluLeuProHisSerProLeuLYsPheHisThrTYrAlaValHisCYsCys 60
Db 256 GACTTTACTGAACTGCCACATTCATTCATGAAATTTCATACCTATGCTGCTCACTGCTGC 315
QY 61 CysPheSerProSerGlyHisIleLeuAlaSerCYsSerThrAspGlyThrValLeu 80
Db 316 TGTTCCTCCCTTCAGACATATTTTGGCATTCGTTCAACAGATGCTACCATGCTCTA 375
QY 81 TrpAsnThrGluAsnGlyIleMetLeuAlaValMetGluGlnProSerGlySerProVal 100
Db 376 TGGAACTAGAAATGAGACAGATGCTGCACTGATGAGACAGCTTACTGACAGCTGCTG 435
QY 101 ArgValCYsGlnPheSerProAspSerThrCYsLeuAlaSerGlyAlaIleAspGlyThr 120
Db 436 AGGTTTGCCAGTTTCCCGACACTCCACGCTTGGCATCAGGGCAGCTGATGGAAT 495
QY 121 ValValLeuThrPheAlaGlnSerTYrLYsLeuTYrArgCYsGlySerValLYsAspGly 140
Db 496 GTGCTTTTGTGATGATGACAGCTCATACAAATTAATGATGCTGATGTTAAAGATGCG 555
QY 141 SerLeuAlaIleCYsAlaPheSerProAsnGlySerPhePheValTYrGlySerSerCYs 160
Db 556 TCTTGGCGGAGTGCATTTTCTCTTAATGAAAGCTTTCTTGACACTGCTCTCATGT 615
QY 161 GlyAspLeuThrValTYrAspAspLYsMetArgCYsLeuHisSerGlyLYsAlaHisAsp 180
Db 616 GGTATTTTAAACAGTGTGATGATTAATAGAGGTCTGATAGTGAAGAAAGCACATGAT 675
QY 181 LeuGlyIleThrCYsAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu 200
Db 676 CTGGAATTAACCTGCTCGATTTTCTTTCACAGCCAGTTTCTGATGAGAAACAAGTCTT 735
QY 201 GlnPhePheArgLeuAlaSerCYsGlyGlnAspCYsGlnValLYsIleTrpIleValSer 220
Db 736 CAGTTTTCGACCTGGCATGCTGTCAGAGATTGCCAAGTCAAATTTGGATTGTTCT 795
QY 221 PheThrHisIleLeu----- 225
Db 796 TTTTACCATATCTTAGGTTTGAATTAATATAAGTACACTGAGTGGGCACTGTGCT 855
QY 225 ----- 225
Db 856 CTTGTTCTGGCTGTGCTTTTCCCATGATGGCAGATGCTAGTCTCAGGGTCAGTGAT 915
QY 225 ----- 225
Db 916 AAGTCTGTCATAGTATATGATTAATACTGAGAAATTAATTCTTCAACATTGACTCAGCAC 975
QY 225 ----- 225
Db 976 ACCAGGATATGCACAACTTGCTTTTGCACTTAATACCTTTTACTTGCTACTGCTTCA 1035
QY 226 ----- 226
Db 1036 ATGACAAACAGTGAACATCTGCAATTTGACCTGGAACACTTTCCTCAAGCGC 1095

Alignment Scores:

QY 229 ThrGluHisGluLeuYsgInpHeThrGluAspTrpSerGluGluVal1SerThrTrp 248
Db 1096 ACAGACATCAGCTGAGCAATTTACCGAGATGGTCAGAGAGATGCTCAACATGG 1155
QY 249 LeuCyAlaGlnAspLeuYsAspLeuVal1Gly1LeuHeYsMetAsnAn11eAspGly 268
Db 1156 CTTTGTCACAAATATTAAAGATCTTGTTGGTAATTTTCAAGATGAATTAACATGTAGTGA 1215
QY 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspAspLeuYs1le----- 285
Db 1216 AAGAACTGTTGAATCTTACAAAAGAAAGTCTGCTGATGATTTGAAATTTGGCTGGAGT 1275
QY 285 ----- 285
Db 1276 CCTGTGCATGTCATGCTCATGACGACTTCAACCTCTGGGCTCAAGTATCCTCTTA 1335
QY 286 -----GluSerLeuGlyLeuArgSerLysVal1LeuArgLys11eGluGluLeuArg 302
Db 1336 CCTGGGCTCAATCTCTAGACTGCGTAGTAAGTGTGAGAAATTTGAAGAGCTCAGG 1395
QY 303 ThrLysValYsSerLeuSerSerGly1LeProAspGluPhe1LeuCyAspPro1LeuThrArg 322
Db 1396 ACCAAGCTTAAATCCCTTTCTTCAAGAAATCTGATGAATTTATATGTCATTAACACTAGA 1455
QY 323 GluLeuMetLysAspProVal1Lea1SerAspGly1TySerTyrgLysGluAlaMet 342
Db 1456 GAACCTATGAAGAATCCGCTCATGCGATGCGATGCGTATTCATATGAAGAAGCAATG 1515
QY 343 GluAsnTrp1LeuSerLysLysLysArgThSerProMetThrAsnLeuVal1LeuProSer 362
Db 1516 GAAATATTGATGACGCAAAAGAAAGCAAGTCCCAAGTCAATCTTGTTCTTCTTCA 1575
QY 363 AlaValLeuThrProAsnArgThrLeuYsMetAla1LeaAsnArgTrpLeuGluThrHis 382
Db 1576 GCGTACTTACACCAATAGAGACTGTGAATAATGCGCCATCAATAGATGCTGAGACACAC 1635
QY 383 GluLys 384
Db 1636 CAAAG 1641

RESULT 14

US-10-077-111-6
/ Sequence 6, Application US/10077111
/ Publication No. US20020187492A1
/ GENERAL INFORMATION:
/ APPLICANT: Toddernud, C. Gordon
/ APPLICANT: Rillema, Jill
/ TITLE OF INVENTION: TBA
/ FILE REFERENCE: 3053-4114US2
/ CURRENT APPLICATION NUMBER: US/10/077,111
/ CURRENT FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: 60/294,181
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 60/269,366
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 1901
/ TYPE: DNA
/ ORGANISM: MOUSE
US-10-077-111-6

Alignment Scores:

Pred. No.: 2.55e-181 Length: 1901
Score: 1616.50 Matches: 312
Percent Similarity: 72.06% Conservative: 31
Best Local Similarity: 65.55% Mismatches: 40
Query Match: 78.97% Indels: 93
DB: 14 Gaps: 3

US-10-077-111-13 (1-384) x US-10-077-111-6 (1-1901)

QY 1 MetValLysLeu11eHisThrLeuAlaAspHisGly1AspAspVal1AsnCysCyAla1Ape 20
Db 19 ATGTGAGCTGTTGATTCACACGCTGCTGATCAGGGAGTACACTGCTGCTGCTT 78
QY 21 SerPheSerLeuLeuAlaThrCySerLeuAspLysThr1LeuArg1LeuTySerLeuArg 40
Db 79 TCGGCTGCCCTCTGCGCCACCTGCTCTTGAGCAAAACCATCCGCTGATCTCCCTTAAGT 138
QY 41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrrAlaVal1HisCysCy 60
Db 139 GACTTGTGAACTGGCGTACTCCCGCTGAAGTTCCACACCTATCTGTGCATCTGCTG 198
QY 61 CysPheSerProSerGlyHis1LeuAlaSerCysSerThrAspGly1ThrThVal1Leu 80
Db 199 TGTTCACACCTCCAGAGACAGCTTTTAGCATCTGCTCCAGACAGCGGACCGAGTGTCT 258
QY 81 TrpAsnThrGluAsnGly1GluMetLeuAlaVal1MetGluGlnProSerGly1SerProVal 100
Db 259 TGGAGCTGCGACGCGGACACACCTGACCGTGTGGAGACGCGGATGACACCTGCTG 318
QY 101 ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerCysGly1Ala1AspGlyThr 120
Db 319 CGGCTGTGCTTTTCCCGACCTGCTACCTAGCCTCAGGCGCTCCGATGATGATCC 378
QY 121 ValValLeuTrpAsnAlaGlnSerTyrrLysLeuTyrrArgCysGly1SerVal1LysAspGly 140
Db 379 ATGCTTTGTGGATGACACAGACATACAAACTATATAGGTGTGTACTGTCAAGATATGC 438
QY 141 SerLeuAlaAlaCysAlaPheSerProAsnGly1SerPhePheVal1ThrGlySerSerCys 160
Db 439 TCATGTGCTGCTGCTGCTGCTTCTCCGATGAGCGCTCTTTGTCACTGCTCTCTGCGC 498
QY 161 GluAspLeuThrVal1TrpAspAspLysMetArgCysLeuHisSerGly1LysAla1HisAsp 180
Db 499 GGGGACTTGACATGTGGAGTGCAGATGAGGTGTCTACACGCGAAGAGGCGACAGAT 558
QY 181 LeuGly1LeuThrCysCyAspPheSerSerGlnProVal1SerAspGly1GluGlnGlyLeu 200
Db 559 CTGGGATCACCGTGCAGAGCTTTCTCTCAGACCTCTCTCTGGCGGAGAA---GGCCTC 615
QY 201 GlnPhePheArgLeuAlaSerCysGly1GlnAspCysGlnVal1Lys1LeuTrp11Val1Ser 220
Db 616 CAGCTTACCAAGTTGGCGTCACTGTGTCAAAGCTGTGAATCAAACTTGCGGCTGTACT 675
QY 221 PheThr----- 222
Db 676 ATTAACCGGTCTTAGGCTTTGAATTAATAAAGCAACATAAGTGGGCACTGCGCC 735
QY 222 ----- 222
Db 736 CCGTTCGGCCGTGCTTTTTCACATGATGGAANAATGCTTGSCATCGGGTCAAGTGCAT 795
QY 223 -----His1LeuAla1ArgArg 228
Db 796 AAATCTGCATCATATAGTATCGGCGCTCAGAGTGTGCTACACAGCTGACTCAGCAT 855
QY 229 ThrGluHis----- 231
Db 856 ACCAGGATGTTAGCACTTGCGCTTGGACCCACACACTCTTACTTGTCTACTGGTTCA 915
QY 231 ----- 231
Db 916 ATGACAGACAGTGAACATTTGGCAGTTTGAACCTGGAACAACCTTCCCAAGCAGGAGC 975
QY 232 -----GluLeuYsgInpHeThrGluAspTrpSerGluGluVal1SerThrTrp 248
Db 976 ATGACAGACCGCTGAAACATTTCACTGAAGATGTCTCAGAGAGATGTCTTCCTGCTGG 1035
QY 249 LeuCyAlaGlnAspLeuYsAspLeuVal1Gly1LeuHeYsMetAsnAn11eAspGly 268
Db 1036 CTTGCTGTCMAAGCTTGGAAAGCTGTGCGGTATTTTCAAGGCAAAACATCATGATGGG 1095

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Qy 269 LysGluLeuLeuAsnLeuThrLysGluSerLeuAlaAspLeuLysIleGluSerLeu 288
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Db 1096 AAGAACTATTGCACTTCACAAAGAAAGTGGCTGGTGAATTGAAATGAAATCTCTA 1155
289 GlyLeuArgSerLysValLeuArgLysIleGluLeuArgThrLysValLysSerLeu 308
1156 GGGCTGGCAGCAAAAGCTCGAGAGATTAAGAGCTCAGGGCCAGATGATGATTCCTC 1215
Qy 309 SerSerLysIleProAspGluPheIleCysProIleThrArgGluLeuMetLysAspPro 328
1216 TCTTCGGAATCCCTGACGAGTTCATCTGCCCAATACCAAGAACTCATGACAGACCCC 1275
Qy 329 ValIleAspAspGlyTyrSerTyrGluLysGluAlaMetGluAsnTrpIleSerLys 348
1276 GTCATCCCATCAGATGGCTACTCTTACGAGAGAGAGCAATGCAAGCTGGATCCACAG 1335
Db 349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
1336 AAGAAAGCTACGAGACCCCATGCAAAATTTGGCTCTCCCTTCATCGTACTGACCCCAAC 1395
Qy 369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
1396 AGGAACTGAAGAGAGCCATCAACCGATGGCTGGAGACGACAGAAAG 1443
Db

RESULT 15
US-10-956-157-10363
; Sequence 10363, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10363
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10363

Alignment Scores:
Pred. No.: 2,47e-166 Length: 1400
Score: 1489.00 Matches: 294
Percent Similarity: 75.77% Conservative: 0
Best Local Similarity: 75.77% Mismatches: 2
Query Match: 72.74% Indels: 92
DB: 22 Gaps: 1

US-10-077-111-13 (1-384) x US-10-956-157-10363 (1-1400)
Qy 89 LeuAlaValMetGluGlnProSerGlySerProValArgValCysGlnPheSerProAsp 108
Db 2 CTGGCAGTGAAGAAACAGCTAGTGGGCAAGCCCTGAGGGGTTTCCCGCAGAC 61
Qy 109 SerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValValLeuTrpAsnAlaGlnSer 128
Db 62 TCACAGGTGTTGGCATCAGGGGCAAGCTGATGGAAGTGTGTTGTGAATGCACAGTCA 121
Qy 129 TyrLysLeuTyrArgCysGlySerValLysAspGlySerLeuAlaAlaCysAlaPheSer 148
Db 122 TACAAATTATATAGATGTAGTGTAAAGATGGCTCTTGGCGGCATGTGCAATTTTCT 181
Qy 149 ProAsnGlySerPhePheValThrGlySerSerCysGlyAspLeuThrValTrpAspAsp 168
Db 182 CCAATAGGAAGCTCTTTGTACAGTGGCTCCATGATGGTGAATTTAAACAGTGGGATGAT 241
Qy 169 LysMetArgCysLeuHisSerGlyLysAlaHisAspLeuGlyIleThrCysCysAspPhe 188
Db 242 AAAATGAGGTGTCCGCAATAGTGAAGAAACACATGATCTTGGAAATTACCTGCTGGCATTTT 301
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Qy 189 SerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPhePheArgLeuAlaSerCys 208
302 TCTTCACAGCAGATTTCTGTAGAGAAACAGGCTTCAATTTTTCATCGGCAATCATGT 361
Qy 209 GlyLysAspCysGlnValLysIleTrpIleValSerPheThrHisIleLeu----- 225
362 GGTGAGATTTGCCAAGTCAAATTTTGGATGTTCTTTTACCCTATCTTAGGTTTGA 421
Qy 225 ----- 225
Db 422 TTAATAATATAAAGTACACTGAGTGGGCACTGCTCTGCTTCTGCTGTGCTTTTCC 481
Qy 225 ----- 225
Db 482 CAGATGGCAGATGATGATCTAGTCTCAGGGTCAGTGAATAGTCTGTATATATGATACT 541
Qy 225 ----- 225
Db 542 AATACTGAGAAATATACTTACACATTTGACTCAGCACACAGTATGTACAACTTGCT 601
Qy 225 ----- 225
Db 602 TTGCACTAATAACCTTTTACTTGTACTGTTCAATGACAACAAACAGTAAACATCTGG 661
Qy 226 ----- 226
Db 662 CAATTGACCTCGAAGAACCTTTGCCAAGCAAGGGCAGAGAACTGAGCAATCAATTT 721
Qy 237 ThrGluAspTrpSerGluGluValValSerThrTrpLeuCysAlaGlnAspLeuLysAsp 256
722 ACCGAATATTTGGTCAGAGAGAGATGTCTCAACATGCTTTGTGCAACAAGATTTAAAGAT 781
Qy 257 LeuValGlyIlePheLysMetLysAsnIleAspGlyLysGluLeuAsnLeuThrLys 276
782 CTGTGTGTAATTTTCAAGATGAATATCATGATGAGAAAGAACTGGAATCTTACAAAA 841
Qy 277 GluSerLeuAlaAspAspLeuLysIleGluSerLeuLysLeuArgSerLysValLeuArg 296
842 GAAAGTGTGCTGATGATTTGAAATTTGAAATCTCTAGAGCTGCTGATTAAGTCTGAGG 901
Qy 297 LysIleGluLeuLeuArgThrLysValLysSerLeuSerSerGlyIleProAspGluPhe 316
902 AAAATTTAAGAGCTCAGAGACCAAGTTAAATCCTTTCTTCAGGAATTCCTGAGAAATTT 961
Qy 317 IleCysProIleThrArgGluLeuMetLysAspProValIleAlaSerAspGlyTyrSer 336
962 ATATGTCCAATTAAGTAAAGAACTTATGAAAGATCCGTCATCGCATCAGATGGCTATTCA 1021
Qy 337 TyrGluLysGluAlaMetGluAsnTrpIleSerLysLysArgThrSerProMetThr 356
1022 TATGAAAAAGGAAGCAATGGAATAATTTGATCAGCAAAAAAGAAACGTACAGTCCATGACA 1081
Qy 357 AsnLeuValLeuProSerAlaValLeuThrProAsnArgThrLeuLysMetAlaIleAsn 376
1082 AATCTTGTCTCTCTTCAAGCGGTACTTACACCAATATGACTCTGAAATAGCCATCATAT 1141
Qy 377 ArgTrpLeuGluThrHisGlnLys 384
1142 AGATGGCTGGAGACACACAAAAAG 1165
Db
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Search completed: October 25, 2005, 05:40:07
Job time : 749 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 25, 2005, 01:14:43 ; Search time 169 Seconds
(without alignments)
3717.931 Million cell updates/sec

Title: US-10-077-111-13
Perfect score: 2047
Sequence: 1 MWKILHLDHGDVNCFA.....LTPNRKLMKINRWLETHOK 384

Scoring table: BLASTSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QPMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd1
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NCM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=US10077111.QCGN1_1.54.@runat_24102005_072846_8202 -NCPU=6 -ICPU=3
-NO_MMAP -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1978	96.6	1844	4	US-09-620-312D-768
2	234.5	11.5	2359	1	US-08-188-582-4
3	234.5	11.5	2359	1	US-08-646-715-4
4	227	11.1	7028	4	US-09-949-016-4194
5	227	11.1	7028	4	US-09-949-016-4195
6	227	11.1	7042	3	US-09-092-508-1
7	227	11.1	7042	3	US-09-435-115-1
8	227	11.1	7042	3	US-09-098-310-1
9	227	11.1	7042	3	US-09-690-364-21
10	227	11.1	7042	4	US-09-949-016-159
11	227	11.1	7075	3	US-09-092-508-15
12	227	11.1	7075	3	US-09-435-115-15

13	226.5	11.1	2130	4	US-09-620-312D-145	Sequence 145, App
14	220.5	10.8	937	4	US-10-101-464A-251	Sequence 251, App
15	218	10.6	5152	3	US-09-690-364-10	Sequence 10, App
16	217.5	10.6	3747	3	US-09-690-364-17	Sequence 17, App
17	217.5	10.6	7157	4	US-09-949-016-4192	Sequence 4193, App
18	217.5	10.6	7157	4	US-09-949-016-4193	Sequence 4193, App
19	217.5	10.6	7171	4	US-09-949-016-971	Sequence 971, App
20	216	10.6	2152	1	US-08-188-582-17	Sequence 17, App
21	216	10.6	2152	1	US-08-646-715-17	Sequence 17, App
22	203.5	9.9	1246	3	US-09-302-769-22	Sequence 22, App
23	198.5	9.7	2186	3	US-08-184-001-1	Sequence 1, App
24	198.5	9.7	2558	3	US-09-184-001-3	Sequence 3, App
25	195	9.5	7886	2	US-08-751-189-2	Sequence 2, App
26	195	9.5	7886	2	US-09-060-836-2	Sequence 2, App
27	195	9.5	7886	3	US-09-184-445-2	Sequence 2, App
28	193.5	9.5	2369	3	US-09-302-769-20	Sequence 20, App
29	188	9.2	3465	3	US-08-914-999-5	Sequence 5, App
30	187.5	9.2	9991	4	US-09-902-540-1014	Sequence 1014, App
31	187	9.1	1422	4	US-09-248-796A-4567	Sequence 4567, App
32	184.5	9.0	1157	4	US-09-270-767-14727	Sequence 14727, App
33	184.5	9.0	1731	4	US-09-902-540-1920	Sequence 1920, App
34	183.5	9.0	1548	4	US-09-614-221A-136	Sequence 136, App
35	182	8.9	2481	3	US-08-899-578-1	Sequence 1, App
36	180.5	8.8	1698	4	US-09-902-540-8422	Sequence 8422, App
37	180.5	8.8	6553	4	US-09-902-540-885	Sequence 885, App
38	180	8.8	1182	4	US-09-248-796A-4568	Sequence 4568, App
39	178.5	8.7	1542	4	US-09-949-016-1365	Sequence 1365, App
40	176	8.6	1185	4	US-09-248-796A-4600	Sequence 4600, App
41	176	8.6	2272	3	US-09-108-857-1	Sequence 1, App
42	175.5	8.6	1115	1	US-08-190-802A-19	Sequence 19, App
43	175.5	8.6	1115	3	US-08-477-346-19	Sequence 19, App
44	175.5	8.6	1115	3	US-08-473-089-19	Sequence 19, App
45	175.5	8.6	1115	3	US-08-487-072A-19	Sequence 19, App

ALIGNMENTS

RESULT 1
US-09-620-312D-768
Sequence 768, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundang
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radje T.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
FILE REFERENCE: 784CIPB2B
CURRENT APPLICATION NUMBER: US/09/620,312D
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Fl_genes Version 1.0
SEQ ID NO 768
LENGTH: 1844
TYPE: DNA

ORGANISM:	Homo sapiens	
FEATURE:		
NAME/KEY:	CDS	
LOCATION:	(164) . (1594)	
US-09-620-312D-768		
Alignment Scores:		
Pred. No.:	2,44e-230	
Score:	1978.00	
Percent Similarity:	80.25%	
Best Local Similarity:	80.25%	
Query Match:	96.63%	
DB:	4	
	Gaps: 1	
US-10-077-111-13 (1-384) x US-09-620-312D-768 (1-1844)		
OY	1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCyCyAlaPhe	20
Db	164 ATGGGAAACATGATTCACACATAGCTGATCATGGGAGAGATGTCAACTGTGCTTC	223
OY	21 SerPheSerLeuLeuAlaThrCySerSerLeuAspLysThrIleArgHeuTySerLeuAsp	40
Db	224 TCCCTTTCCCTTTGGCTACTTGGCTCTTGGACAAACAACTTGCCTGATCTTACCT	283
OY	41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCyCyS	60
Db	284 GACTTTACTGAACCTGCACATCTCCATTCGAGTTTCATACCTATGCTGCCACTGCTGC	343
OY	61 CysPheSerProSerGlyHisIleLeuAlaSerCySerThrAspGlyThrThrValLeu	80
Db	344 TGTTCCTCCCTTCAGACATATTTGGCATGTGTCAACAGATGATCCACTGTCTTA	403
OY	81 TrpAenThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
Db	404 TGGATATCTGAAATAGGACAGATGCTGGCAGATGATGAACAGCTTATGGCAGCCCTTG	463
OY	101 ArgValLysGlnPheSerProAspSerThrCyGluAlaSerGlyAlaAlaAspGlyThr	120
Db	464 AGGGTTTGGCAGATTTTCCCACTCCACAGTGTGGATTCAGGGGCACTGATGGAACCT	523
OY	121 ValValIleuTrpAsnAlaGlnSerTyrLysLeuTyrArgCyGlySerValLysAspGly	140
Db	524 GTGGTTTGTGGAAATGCCACAGTCATCAAAATTATATAGATGTGTGTTAAAGATGCC	583
OY	141 SerLeuAlaAlaCyAlaPheSerProAsnGlySerPhePheValThrGlySerSerCyS	160
Db	584 TCCCTGGCGCGCATGTGCATTTTCTCCTAATGGAAGCTTTTGTCTCACTGGCTCCATAT	643
OY	161 GlyAspLeuThrValTrpAspAspLysMetArgCysLeuHisSerGlyLysValAsnIAsp	180
Db	644 GGTGATTTTACAGTGTGGATGATTAAGAAGTGTCTGCATATGTAAAAAGCACATGAT	703
OY	181 LeuGlyIleThrCyAspAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeu	200
Db	704 CTTCGAATTAACCTGTGCGCATTTTCTTCTTCCACAGCCAGTTTTCGATGGAGAACAGTCTT	763
OY	201 GlnPhePheArgLeuAlaSerCyGlyGlnAspCyGlnValLysIleTrpIleValSer	220
Db	764 CAGTTTCTTTCGACTGCGCATCATGTGTGTCAGGATTCGCAAGTCCAAATTTGGATGTTTCT	823
OY	221 PheThrHisIleLeu-----	225
Db	824 TTTTACCATATCTTTAGCTTTTGAAATTAAATATTAAGAATACACTGATGGGCACTGTGCT	883
OY	225 -----	225
Db	884 CCTGTTCTGGCTTGTGCTTTTCCCATGATGGGACAGATGCTAGTCTCAGGGTCAGTGAT	943
OY	225 -----	225
Db	944 AAGTCTGTCAATGATATATGATACTAATTAAGAAATATACTGAGAAATATCTTCACACATTGACTCAGCAC	100
OY	225 -----	225

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Db      1004 ACCAGGATATGACAACTTGTGCTTTGGACACTAATACCTTTACTTGCTACTGGTTCA 1063
QY      226 -----AlaArgArg 228
Db      1064 ATGACACAAAACAGTGAACATCTGGCAATTTGACCTGGMAACACTTTGCCAAGGAGGC 1123
QY      229 ThGluHnIeGiInLeuLySgInPhoThGluAspTrpSerGluGluValValIseThTrp 248
Db      1124 ACACAACATCAGCTGAAGCAATTTACCGAAGATTGGTCAGAGGAGCATGTCCTCAACATTGG 1183
QY      249 LeuCySaIaGInAspLeuLySAspLeuValGlyIlePheLeuSWeAsnAnIlaAspGly 268
Db      1184 CTTTGTCGACAAAGATTTAAAGAATCTGTGGATATTTCGAAGATGAAATTAACATTGATGGA 1243
QY      269 LysGluLeuLeuAsnLeuThrLysGluIseLeuAlaAspAspLeuLyIleGluIseLeu 288
Db      1244 AAGAACTGTTGAATCTTACAAAAGAAAGCTGGCTGATGATTTGAATAATTGAATCTCTA 1303
QY      289 GlyLeuArgSerLysValLeuArgValIleGluGluLeuArgThrLysValLysSerLeu 308
Db      1304 GGACTGGGATATAAGGCTGAGGAAAAATTGAAGAGCTCAGAGACCAAGTTAAATCCCTT 1363
QY      309 SerSerGlyIleProAspGluPheIleCySProIleThrArgGluLeuMetLysAspPro 328
Db      1364 TCTTCAGGAATCTCGTAGAATTTATATATGTCCAATTACTAGAAACCTTAGAAAGATCCG 1423
QY      329 ValIleAlaSerAspGlyIlyTrSerTyrGluLysGluAlaMetGluAntTPIIleSerLys 348
Db      1424 GTCATCCATCCATGAGTGCCTATTCTATATGAAGAAAGAACCAATGCAAAATTTGATCAGCAA 1483
QY      349 LysLysArgThrSerProMetThrAsnLeuValLeuProSerAlaValLeuThrProAsn 368
Db      1484 AAGAAAGCTACAGATCCCATGACAAATCTTGTTCTTCTTCAGGGGATCTTACACCAAT 1543
QY      369 ArgThrLeuLysMetAlaIleAsnArgTrpLeuGluThrHisGlnLys 384
Db      1544 AGGACTGTGAATAATGGCCATCAATATAGATGGCTGGAGACACACCAAAG 1591

RESULT 2
US-08-188-582-4
: Sequence 4, Application US/08188582
: Patent No. 5534410
: GENERAL INFORMATION:
:   APPLICANT: Tjian, Robert
:   APPLICANT: Comati, Lucio
:   APPLICANT: Dynalac, Brian D.
:   APPLICANT: Hoey, Timothy
:   APPLICANT: Rupprecht, Siegfried
:   APPLICANT: Tanese, Naoko
:   APPLICANT: Wang, Edith
:   APPLICANT: Weinzierl, Robert O.J.
:   TITLE OF INVENTION: YATA-BINDING PROTEIN ASSOCIATED FACTORS,
:   NUMBER OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
:   NUMBER OF SEQUENCES: 36
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: FLEHR, HOHBACH, TEST, ALARITTON & HERBERT
:   STREET: 4 Embarcadero Center, Suite 3400
:   CITY: San Francisco
:   STATE: California
:   COUNTRY: USA
:   ZIP: 94111-4187
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patentin Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/188,582
:   FILING DATE: 28-JAN-1994
:   CLASSIFICATION: 435
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Osman, Richard A
:

```

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: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELE: 910 277299
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2359 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 49..2160
: US-08-188-582-4

Alignment Scores:
Pred. No.: 1,21e-17 Length: 2359
Score: 234.50 Matches: 88
Percent Similarity: 44.34% Conservative: 49
Best Local Similarity: 28.48% Mismatches: 128
Query Match: 11.46% Indels: 45
DB: 1 Gaps: 11

US-10-077-111-13 (1-384) x US-08-188-582-4 (1-2359)
QY 3 Lysleu1le1h1sthr1leu1ala1asp1h1s1gl1y1asp1asp1alancys1cys1ala1phe1ser--- 21
Db 1369 GAGGTAAACCAAGACCTTAATGCTACACCGGACCCGATACCCCTGCTGCTTGGCCCC 1428
QY 22 ---Phe1ser1leu1leu1a1thr1cys1ser1leu1asp1sthr1leu1g1leu1yr1ser1leu1arg 40
Db 1429 GAGATGAACCTGCTCTCTCATGTTCCAGACAGCACCAATAGCTGTGCTCTCTC 1488
QY 41 Asphe1thr1glu1leu1p1ro1h1ser1p1ro1leu1ysp1he1sthr1y1al1val1h1cys1cys 60
Db 1489 ACCGTGTCCTGCGTA-----GTCACTACCCGCGGACGCTTTACCGGTGTGGAGATT 1542
QY 61 Cys1phe1ser1p1ro1ser1gl1h1s1le1leu1ala1ser1cys1ser1th1asp1gl1y1thr1val1leu 80
Db 1543 CGCTTTCGCGCGGACTACTATTGTTCTTCTTCTGTCAGCAAAAGCTCGTCTG 1602
QY 81 Thr1asn1thr1glu1asn1gl1met1leu1ala1val1met1glu1n1p1ro1ser1gl1y1ser1p1roval 100
Db 1603 TGGCCACCGGATTCATCAAGCCGTGGCGCTATTCGTGGCTCACTTG---TCCGACGTG 1659
QY 101 Arg1val1cys1gl1n1phe1ser1p1ro1asp1ser1thr1cys1leu1ala1ser1gl1y1ala1asp1gl1ythr 120
Db 1660 GATTGTGTAATTCATCCCAATTCATTAATGTGGCCACGGGTTCTAGCGATCGCAG 1719
QY 121 Val1val1leu1tr1pas1nal1ag1n1ser1tyr1lys1leu1tyr1arg1cys1gl1y1ser1val1lys1asp1gl1y 140
Db 1720 GTACGCGCTGTGGACACATGACCGGTCAGTCGGAGCCGCTTAGAGACGGCCACAGGGA 1779
QY 141 Ser1leu1ala1acys1ala1phe1ser1p1ro1asn1gl1y1ser1phe1p1e1val1thr1gl1y1ser1cys 160
Db 1780 TCGGTGAGTTCTCTCGCCCTTCGCGCTGCGCGGATCTGGGCTCGGGTTCAGTAGAT 1839
QY 161 Gly1asp1leu1thr1val1tr1pas1p---Asp1lys1met1arg1cys1leu1h1s1ser1gl1ly1al1h1s 179
Db 1840 CACAATTCATCATCTGTGGATCTGTCCAGACGATCCCTGGTCACACCCCTTTGAGGCAC 1899
QY 180 Asp1leu1gl1y1leu1thr1cys1asp1phe1ser1ser1gl1n1p1roval1ser1asp1gl1y1glu1n1gl1y 199
Db 1900 ACTAGCACTGACACAGATCACCTTAGT-----CGGATGGAAGACGTG--- 1944
QY 200 Leu1gl1n1phe1p1e1arg1leu1ala1ser1cys1gl1y1glu1n1p1roval1ys1le1tr1p1le1val 219
Db 1945 -----CTGGCTGCAGCCGCTTGATTAACAATCAATCTGTG----- 1983
QY 220 Ser1phe1thr1h1s1le1leu1ala1arg1arg1thr1glu1h1gl1n1leu1ys1gl1n1phe1thr1glu1n1p 239
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Db 1984 -----GACTTGCACAAGCTTTACGGAAGAC
QY 240 Trp1ser1glu1n1val1ser1thr1tr1ple1cys1al1ag1n1asp1leu1ys1asp1leu1al1gl1y 259
Db 2008 TATATCAGCAATCAATC---ACTGTCTCCACCATTCAGATGAGACGAC---GAGCAG 2061
QY 260 Ile1phe1ys1met1arg1asn1leu1asp1gl1y1leu1glu1-----Leu1leu1asn1leu1thr 275
Db 2062 GTTACTCTCATGCGGATCTTCCCGACAGAACTCCGCAATTTGTACCTGCACTTACG 2121
QY 276 Lys1glu1ser1leu1ala1asp1-----Asp1leu1ys1ile1glu1ser 287
Db 2122 CGCCAAATCTCTGATGTGCGGTGGGTCTATTCAGAGTTAGAGACAGATTAAGCTTA 2180
QY 288 Leu1gl1y1leu1arg1ser1lys1val1leu1arg 296
Db 2181 TTGTGTAATCAATGATGATGATTAAGG 2207

RESULT 3
US-08-646-715-4
: Sequence 4, Application US/08646715
: Patent No. 5637686
: GENERAL INFORMATION:
: APPLICANT: Tjian, Robert
: APPLICANT: Comai, Lucio
: APPLICANT: Dynlacht, Brian D.
: APPLICANT: Hoey, Timothy
: APPLICANT: Ruppert, Siegfried
: APPLICANT: Tanese, Naoko
: APPLICANT: Weinzierl, Robert O.J.
: TITLE OF INVENTION: "TATA-BINDING PROTEIN ASSOCIATED FACTORS,
: TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAIFS AND METHODS OF USE
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,715
: FILING DATE: 09-MAY-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/188,582
: FILING DATE: 28-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELE: 910 277299
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2359 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 49..2160
: US-08-646-715-4
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Alignment Scores:

Pred. No.:	1 21e-17	Length:	2359
Score:	234.50	Matches:	88
Percent Similarity:	44.34%	Conservative:	49
Best Local Similarity:	28.48%	Mismatches:	128
Query Match:	11.46%	Indels:	45
DB:	1	Gaps:	11

US-10-077-111-13 (1-384) x US-08-646-715-4 (1-2359)

QY	3	LysLeuLleHisThrLeuAlaAspHisGlyAspAspValAsnCysValaPheSer---	21
DB	1369	GAGGTAAACGAGAGCTTAATGGGTCACACCGGACCCCTTAATACCGCTTGCTGCCCTTACCC	1428
QY	22	---PheSerLeuLeuAlaThrCysSerLeuAspLysThrLeuArgLysLeuArg	40
DB	1429	GAGATGAACCTGTGCTCTATGTTCCGAGAGACGACCAATAGGCTGTGCTGCTGCTC	1488
QY	41	AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys	60
DB	1489	ACCTGCTCCGCGTA-----GTCACCTACCGCGGACGTTTACCGGTGGGATGTT	1542
QY	61	CysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThrValLeu	80
DB	1543	CGCTTTCGCGCGCATGCTACTATTGTTCTTGTTCGTACGACAAACTGCTGCTG	1602
QY	81	TyrAsnThrGluAsnGlyGlnMetLeuAlaValMetGluGlnProSerGlySerProVal	100
DB	1603	TGGGCCACGGATTCATCAATCAAGCGCTTGGGATTCCTGGGTCACTTG---TCGACGTG	1659
QY	101	ArgValCysGlnPheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThr	120
DB	1660	GATTGTACAAATTTCATCCCAATTTCATTAATGTGCGCACCGGTTCTAGCATCGCACG	1719
QY	121	ValValLeuThrPheAlaGlnSerTyrLysLeuTyrArgCysGlySerValLysAspGly	140
DB	1720	GTCACGCTGTGGGACACATGACGCGTCAGTCGGTACCGCTGATGACGGGCCAACAGGA	1779
QY	141	SerLeuAlaIleCysAlaPheSerProAsnGlySerPheValThrGlySerSerCys	160
DB	1780	TGGGTGATGTTCTGCGCTTCTCCGCTGGCGCGGATTCGGCTGGGTTCTAGTAT	1839
QY	161	GlyAspLeuThrValTyrAsp---AspLysMetArgCysLeuHisSerGlyLysAlaHis	179
DB	1840	CACAAATCATCATCTGGATCTGTGACAGGATCCCTGGTACACCCGTTGAGGCAC	1899
QY	180	AspLeuGlyIleThrCysAspPheSerSerGlnProValSerAspGlyGluGlnGly	199
DB	1900	ACTAGCACTGTGACACGATCACCTTACG-----CGCGATGGAACAGTC--	1944
QY	200	LeuGlnPheThrArgLeuAlaSerCysGlyGlnAspCysGlnValLysIleTyrIleVal	219
DB	1945	-----CTGGCTGACGCGGCTTGGATACATCTTAACCTCTGTG-----	1983
QY	220	SerPheThrHisIleLeuAlaArgArgThrGluHisGlnLeuLysGlnPheThrGluAsp	239
DB	1984	-----GACTTTCACAGGTTTACCGAAGAC	2007
QY	240	TyrSerGluGluValIleSerThrTyrLeuCysAlaGlnAspLeuLysAspLeuValGly	259
DB	2008	TATATCAGCAATCATC---ACTGTGTCCACCATCAGATGAGAACGAC--GAGGAC	2061
QY	260	IlePheLysMetAsnAsnIleAspGlyLysGlu-----LeuLeuAsnLeuThr	275
DB	2062	GTTACTCTCTGCTACTTCCCGACGAAACTCGCATTTGTACCTGACCTTTTACG	2121
QY	276	LysGluSerLeuAlaAsp-----AspLeuLysIleGluSer	287
DB	2122	CGCGAAATCTGCTCC--GATGTGCGGTGGGTATTCAGAGTTTGAAGACAGATTAAGCTTA	2180
QY	288	LeuGlyLeuArgSerLysValLeuArg	296

DB 2181 TTGTATACGATATGATGTTAAGG 2207

DB	US-09-949-016-4194	Sequence 4194, Application US/09949016
DB	Patent No. 6812339	GENERAL INFORMATION:
DB	APPLICANT: VENTER, J. Craig et al.	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
DB	TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	FILE REFERENCE: CL001307
DB	CURRENT APPLICATION NUMBER: US/09/949,016	CURRENT FILING DATE: 2000-04-14
DB	PRIOR APPLICATION NUMBER: 60/241,755	PRIOR FILING DATE: 2000-10-20
DB	PRIOR APPLICATION NUMBER: 60/237,768	PRIOR FILING DATE: 2000-10-03
DB	PRIOR APPLICATION NUMBER: 60/231,498	PRIOR FILING DATE: 2000-09-08
DB	NUMBER OF SEQ ID NOS: 207012	SOFTWARE: FastSeq for Windows Version 4.0
DB	SEQ ID NO 4194	LENGTH: 7028
DB	TYPE: DNA	ORGANISM: Human
DB	US-09-949-016-4194	

Alignment Scores:

Pred. No.:	6.63e-16	Length:	7028
Score:	227.00	Matches:	102
Percent Similarity:	40.24%	Conservative:	63
Best Local Similarity:	24.88%	Mismatches:	140
Query Match:	11.09%	Indels:	105
DB:	4	Gaps:	19

US-10-077-111-13 (1-384) x US-09-949-016-4194 (1-7028)

QY	3	LysLeuLleHisThrLeuAlaAspHisGlyAspAspValAsnCysValaPheSerPhe	22
DB	2612	GAACTAGTACAGCCATATGATGAGCACTCAGAGCAAGTCAATTGCGCTTACACCAAC	2671
QY	23	Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSer	38
DB	2672	AGTAGCATCATCTTCTTACGCACTGGGTCAAGTCACTGCTTCTTCAAACTTTGGGAT	2731
QY	39	LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHis	56
DB	2732	TTCATCAAA-----AAAGATGTGAAATACCATGTGTTGTCATCAAAATTCAGTCAAT	2785
QY	59	CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr	78
DB	2786	CAGTGCAGATTTTTCACACAGATGATAGCTTTTGGCTTAAGTTTACACTGATGMACTTA	2845
QY	79	ValLeuThrAsnThrGluAsnGly-----GlnMetLeu	89
DB	2846	AMCCTTTGGGATGCGCATCAGCAATGAGAGAAAGCATTAATGTGAACAGTTCTTTC	2905
QY	90	AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer	106
DB	2906	CTTAATTTGGAGACCTTCAAGAGCATATGCAAGTATGTGTAAGTTGTTGCTGCTGCT	2965
QY	107	ProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValValLeuThrPheAla	126
DB	2966	GCGATGAGGCGAAGATATATGCG---GCAGCAAAAATAAATACTTTTGGGATTAACA	3022
QY	127	GlnSer---TyrIleLeuTyrArgCysGlySerValLysAspGlySerLeuAla-----	143
DB	3023	GACTCAGTTCAAAAGGTGCTGATTGC-----AGAGGACATTTAAGTTGGGTT	3070
QY	144	---AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp	162
DB	3071	CATGCTGATGATGTTTCTCTCATGATGATCATTTTTCACATCTTCTGATGACCAAGACA	3130

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Qy      163 LeuThrValTrpAspAspIleMetArgCysLeuHisSer----- 175
      :::::|||||
Db      3131 ATCAGGCTCTGGAGACAAAGAAAGTATGTAAAGAACTGCTGTAAATGTTAAAGCAAGA 3190
Qy      175 ----- 175
Db      3191 GTAGATGTGTGTTTCAAGAAATGAAGTATGTCCTTGCAAGTTGACCATATAGACGT 3250
Qy      176 -----GluysalAhIsAspLeuGlyIleThr 184
      176 -----
Db      3251 CTGCAACTCATTAATGAGAAACAGTCAGATTGATTAATCTGACTGAAGCTCAAGTTAGC 3310
Qy      185 CysCysAspPheSerSerGlnProValSerAspGlyGlnGlyLeuGlnPhePheArg 204
      |||||
Db      3311 TGCTGTGCTTAAGTCCACAT-----CTTCAGTAC----- 3340
Qy      205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSerPheThrHisIle 224
      ::|||
Db      3341 ATTCGATTGTGAGATGAAGAAATGAGCCATGTGAGATTGAACCTGTAAACATAGAAATC 3400
Qy      225 LeuAlaArgArgThrGlnHisGlnLeuLys-----GlnPheThrGluAspTrp 240
      |||||
Db      3401 TTCAGTCCAGGTTTCAGCACAGAAACGTGATGACATCCAGTTCCACAGCCGAT--- 3457
Qy      241 SerGluGluValIleSerThrTrpLeuCysAlaGlnAsp-LeuLysAspLeuValGlyIle 260
      :::::|||||
Db      3458 GAGAAAGACTTATTATTCACAT-----TCTATGATGCTGAATTCAGATTCAGATGAAAT 3508
Qy      260 ePheLysMetAsnAsnIleAspGlyLysGluLeuLysAsnLeuThrLysGlnSerLeuAla 280
      ::|||
Db      3509 TGGCAATGTGACAAATGTATCTTTCTACAGAGCCATCAGAAACAGTGAAGACTTAA- 3566
Qy      280 AlaAspAspLeuLysIleGlnSerLeuGlyLeu-----ArgSerLys 293
      ::|||
Db      3567 -GACTCTTGAAGAAATTCAGACCTGCTTCTTGTCATTGATGAGAACAGTGAAGTATGC 3625
Qy      293 sValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeuSer----- 309
      ::|||
Db      3626 AATATTA-----TTACTGGAATTAAGAAAGAAAGCTTGTCTGTCCACAGGTAACAGTA 3679
Qy      310 -----SerGlyIleProAspGluPheIleCysProIleThrArgI 323
      ::|||
Db      3680 CTTTCTGTGACATTTCACGATGCTACCA--AGTTTCATCTACCTGCTGACAAAG 3736
Qy      323 uLeuMetLysAspProValIleAlaSer 332
      ::|||
Db      3737 ACTGCAAGATCTGAGATTGATCTCC 3764

RESULT 5
US-09-949-016-4195
: Sequence 4195, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4195
: LENGTH: 7028
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-4195

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Alignment Scores:
Pred. No.: 6,63e-16 Length: 7028
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: 4 Gaps: 19

US-10-077-111-13 (1-384) x US-09-949-016-4195 (1-7028)
Qy      3 LysLeuIleHisThrLeuAlaAspAspIleGlyAspAspValAsnCysCysAlaPheSerPhe 22
      ::|||
Db      2612 GAACATGACACACCTATGATGACACCTCAGACAGACATTCCTGCATTTTCCACCAAC 2671
Qy      23 Ser-----LeuAlaIleThrCysSerLeuAspLysThrIleValGlyLeuSer 38
      ::|||
Db      2672 AGTATGATCATCTTCTCTTACCCACGCGGCAAGTACGCTTCCTCAACCTTGGGAT 2731
Qy      39 LeuArgAspPheThrGlnLeuProHisSerProLeuLysPheHisThrTyAlaValHis 58
      ::|||
Db      2732 TTGATACAA-----AAGAAATGCGAAATTCAGTTGCTCATACAAATTCAGTCAAT 2785
Qy      59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78
      ::|||
Db      2786 CACTGACAGATTTTCACACAGATGATAGACTTTTGGCTAGTTCTTTCAGCTGATGAACTTA 2845
Qy      79 ValLeuTrpAsnThrGlnLeuGly-----GlnMetLeu 89
      ::|||
Db      2846 AAGCTTTGGATGCGACATCAGCAATGAGAGAAACATTAATGTGAACAGTTCTTC 2905
Qy      90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
      ::|||
Db      2906 CTAATTTGACAGACCTTCAAGAGAGATATGAGATAGTGAAGTGTGCTGCTGCT 2965
Qy      107 ProAspSerThrCysLeuAlaSerGlyAlaAlaAspLysThrValLeuTrpAsnAla 126
      ::|||
Db      2966 GCTATGATGTCAGAGATATATGCTG--GACAGCAAAATTAATCTTTTGTGAAATACA 3022
Qy      127 GlnSer---TyrLysLeuTyArgCysGlySerValLysAspGlySerLeuAla----- 143
      ::|||
Db      3023 GACTCAGCTTCAGAGCGGCTGATTC-----AGAGACATTTAAAGTTGGGTT 3070
Qy      144 ---AlaCysAlaPheSerProAsnGlySerPhePheValThrGlnLysSerCysGlyAsp 162
      ::|||
Db      3071 CATGCTGATGATTTTCTCTGATGATCATCATTTTTCACATCTTCTGATGACCAACA 3130
Qy      163 LeuThrValTrpAspAspIleMetArgCysLeuHisSer----- 175
      ::|||
Db      3131 ATCAGGCTCTGGAGACAAAGAAAGTATGTAAAGAACTGCTGTAAATGTTAAAGCAAGA 3190
Qy      175 ----- 175
Db      3191 GTAGATGTGTGTTTCAAGAAATGAAGTATGTCCTTGCAAGTTGACCATATAGACGT 3250
Qy      176 -----GluysalAhIsAspLeuGlyIleThr 184
      176 -----
Db      3251 CTGCAACTCATTAATGAGAAACAGTCAGATTGATTAATCTGACTGAAGCTCAAGTTAGC 3310
Qy      185 CysCysAspPheSerSerGlnProValSerAspGlyGlnGlyLeuGlnPhePheArg 204
      |||||
Db      3311 TGCTGTGCTTAAGTCCACAT-----CTTCAGTAC----- 3340
Qy      205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSerPheThrHisIle 224
      ::|||
Db      3341 ATTCGATTGTGAGATGAAGAAATGAGCCATGTGAGATTGAACCTGTAAACATAGAAATC 3400
Qy      225 LeuAlaArgArgThrGlnHisGlnLeuLys-----GlnPheThrGluAspTrp 240
      |||||
Db      3401 TTCAGTCCAGGTTTCAGCACAGAAACGTGATGACATCCAGTTCCACAGCCGAT--- 3457
Qy      241 SerGluGluValIleSerThrTrpLeuCysAlaGlnAsp-LeuLysAspLeuValGlyIle 260
      ::|||
Db      3458 GAGAAAGACTTATTATTCACAT-----TCTATGATGCTGAATTCAGATGATGAAAT 3508

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QY 260 ePhelyMeuAsnAenlleaspGlyLysGluLeuLeuAsnLeuThrlyGluSerLeuAl 280
 Db 3509 TGGCAATTGGACAAATATATCTTTCTACAGGCCATCAGCAAGAAACGTAAGACTTTA-- 3566
 QY 280 AASPAPLeuLylleGluSerLeuGlyLeu-----ArgSerly 293
 Db 3567 -GACTCTTGAATAATTCAGACTCTTTCTGTCATTGTGATGAGACAGTGAAGTATGG 3625
 QY 293 nValleuAArglyleGluGluLeuAArgThrlyVallySerLeuSer----- 309
 Db 3626 AATATTA-----TTACTGAAATTAAGAAAAGACTTTGTCTGTACCAAGGTACAGTA 3679
 QY 310 -----SerGlyleProaspGluPheleCySerProileThrArgAl 323
 Db 3680 CTTTCTTGATGACATTCTCAGACGATCAACA---AGTTTCATCTACTCTGCTGACAG 3736
 QY 323 uLeuMeLlyAspProValleAlaSer 332
 Db 3737 ACTGCAAAAGATCTGAGCTTTGATCTCC 3764

RESULT 6

US-09-092-508-1
 ; Sequence 1, Application US/09092508
 ; Patent No. 6291643
 ; GENERAL INFORMATION:
 ; APPLICANT: Honzel, William J.
 ; TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 ; STREET: 3100 No. 6291643west Center, 90 South Seventh St
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/092,508
 ; FILING DATE: 05-JUN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/048,807
 ; FILING DATE: 05-JUN-1997
 ; APPLICATION NUMBER: 60/055,258
 ; FILING DATE: 07-AUG-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kettelberger, Ph.D., Denise M
 ; REGISTRATION NUMBER: 33,924
 ; REFERENCE/DOCKET NUMBER: 11669.6USUI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-332-5300
 ; TELEFAX: 612-332-9081
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7042 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 578...4159
 ; OTHER INFORMATION:
 ; US-09-092-508-1

Alignment Scores: 6.65e-16 Length: 7042
 Rred. No.:

Score: 227.00 Matches: 102
 Percent Similarity: 40.24% Conservatlyc: 63
 Best Local Similarity: 24.88% Mismatches: 140
 Query Match: 11.09% Indels: 105
 DB: 3 Gaps: 19

US-10-077-111-13 (1-384) x US-09-092-508-1 (1-7042)

QY 3 LyeLeuLleHleThrLeuAlaAspHleGlyAspAspValleAsnCySerVallePheSerPhe 22
 Db 2612 GAACCTAGTACACACCTATGATGACACTCAGACCAAGTCAATTCGCTCCATTTCACCAAC 2671
 QY 23 Ser-----LeuLeuAlaThrCySerSerLeuAspLyThrleAArgLeuTySer 38
 Db 2672 AGTAGCATCATCTTCTCTTAGCCACTGGGTCAAGTACAGTCTGCTCTCAAACTTTGGAT 2731
 QY 39 LeuAArgAspPheThrGluLeuProHleSerProLoullySerPheHleThrTyAlaValleHis 58
 Db 2732 TTGAATCAA-----AAAGAAATGCGAAATACCATGTTTGTCATACAAATTCAGTCAAT 2785
 QY 59 CySerCySerPheSerProSerGlyHleleLeuAlaSerCySerThrAspGlyThrTr 78
 Db 2786 CACTGCAGATTTTCACCAAGTCAATGAGCTTTTGCTAGTTGTTTCAGCTGATGAAACCTTA 2845
 QY 79 ValleuThrAsnThrGluAsnGly-----GlnMeLeu 89
 Db 2846 AAGCTTTGGGATCGCATCAGCAATGAGAGGAAAGCAATTAATGAAACAGTTCTTC 2905
 QY 90 AlaValMeGluGlnProSerGlySerPro-----ValleGlyValCyGlnProSer 106
 Db 2906 CTAATTTTGAGAGACCCCTCAAGAGATATGAGATGATGATGATGATGATGATGATGATGAT 2965
 QY 107 ProAspSerThrCySerLeuAlaSerGlyAlaAlaAspGlyThrValleuThrAspAla 126
 Db 2966 GCTGATGTGTCAGCAAGATATGCTG---GCGCAAAAATAATTAATCTTTTGTGATATAC 3022
 QY 127 GlnSer---TyrlySeruTyArgCySerGlySerValleuAspGlySerLeuAla----- 143
 Db 3023 GACTCAGCTTCAAAAGGCGGTGATTC-----AGAGCATTTTAAGTTGGGT 3070
 QY 144 ---AlaCyAlaHleSerProAsnGlySerPhePheValleThrlyGlySerCyGlyAsp 162
 Db 3071 CATGTGTGATGATGTTCTCTGATGATCATCATTTTTCACATCTTCTGTATGACACAGACA 3130
 QY 163 LeuThrValleThrAspAspLySerGlySerGlyLeuHisSer----- 175
 Db 3131 ATCAGGCTCTGGAGACAAAGAAAGATATGTAAGAACTCTGCTTAATGTAAGCAAGAA 3190
 QY 175 ----- 175
 Db 3191 GTAGATGTTGTTTTCAGAAATAATGAAGTATGCTCTTGCAGAGTGAACCATATAGACGT 3250
 QY 176 -----GlnlySerAlaHisAspLeuGlyleThr 184
 Db 3251 CTGCAATCTTAATGAGAAACAGCTCAGATTGATTATCTGACTCAAGCTCAAGTAAAG 3310
 QY 185 CySerAspPheSerSerGlnProValleAspGlyGluGlnGlyLeuGlnPhePheAs 204
 Db 3311 TGCTGTGCTTAAGTCCACT-----CTTCAGTAC----- 3340
 QY 205 LeuAlaSerCySerGlyAspGlyAspGlyValleThrlyleValleAspPheThrHis 224
 Db 3341 ATTGCATTTGAGAGATGAATAATGAGCATTGAGATTTTGAAGCTTGAACCAATAGATTC 3400
 QY 225 LeuAlaArgArgThrGluHleGlnLeuLyS-----GlnPheThrGluAspTrp 240
 Db 3401 TTCAGTCCAGGTTTCAGCACAAGAAACTGTATGACATTCACATTCACAGCCGAT-- 3457
 QY 241 SerGluGluValleValleSerThrTrPleuCyAlaGlnAsp-LeuLyAspLeuValleGly 260
 Db 3458 GAGAGAGCTCTTATTCAGT-----TTCGATGATGCTGTGAATTCAGGATGAGAT 3508
 QY 260 ePhelyMeuAsnAenlleaspGlyLysGluLeuLeuAsnLeuThrlyGluSerLeuAl 280

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Db      3509 TGGCAATTGACAAATGATCTTTCTACAGCCATCAGAAACAGTGAAGACTTTA-- 3566
Qy      280 aAspAspLeuLysIleGluSerLeuGlyLeu-----ArgSerLy 293
Db      3567 -GACTCTTGAAATAATTCAGACTCTTTCTGTGATTTGATGACAGTGAAGGTATGG 3625
Qy      293 sValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeuSer----- 309
Db      3526 AATATTA-----TTACTGAAATTAAGAAAAGACTTTGCTGTCCACAGGTAACGTA 3679
Qy      310 -----SerGlyIleProAspGluPheIleCysProIleThrArgG1 323
Db      3680 CTTTCTTGACATTTCTCAGCATGCTACCA--AGTTTCATCATCTGCTGACAG 3736
Qy      323 uLeuMetLysAspProValIleAlaSer 332
Db      3737 ACTGCAAAAGATCTGAGATTGTGATCTCC 3764

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RESULT 7

US-09-435-115-1

Sequence 1, Application US/09435115

Patent No. 6346607

GENERAL INFORMATION:

APPLICANT: Henzel, William J.

TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: 3100 No. 6346607west Center, 90 South seventh St

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/435.115

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/092.508

FILING DATE: 60/055.258

FILING DATE: 07-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ketelberger, Ph. D., Denise M

REGISTRATION NUMBER: 33,924

REFERENCE/DOCKET NUMBER: 11669.6USU1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 7042 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 578...4159

OTHER INFORMATION:

US-09-435-115-1

Alignment Scores:

Pred. No.: 6.65e-16

Score: 227.00

Percent Similarity: 40.24%

Length: 7042

Matches: 102

Conservative: 63

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Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: 3 Gaps: 19

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US-10-077-111-13 (1-384) x US-09-435-115-1 (1-7042)

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Qy      3 LysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPheSerPhe 22
Db      2612 GAATTAATACACACCTTATGATGACACTCAGAGCAAGTCAATTCCTCCATTACCAAC 2671
Qy      23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTySer 38
Db      2672 AGTAGCATCATCTTCTCTTAGCCACCTGGGTCAAGTCAAGTCACTTCCTCAAACTTGGGAT 2731
Qy      39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyAlaValHis 58
Db      2732 TTGAATCAA-----AAGAAATGTCGAATAACCAATGTTGGCTCATCAAAATTCGTAAT 2785
Qy      59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThrThr 78
Db      2786 CACTGCAGATTTTTCACCAAGATGATTAAGCTTTGGCTAGTTGTTTCAGCTGATGCAACCTTA 2845
Qy      79 ValLeuTrpAsnThrGluAsnGly-----GlnMetLeu 89
Db      2846 AAGCTTGGATGCGACATCAGCAAAATGAGAGAAACATTAATGTAAGAACGTTCTTC 2905
Qy      90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
Db      2906 CTAAATTTGAGAGCACTCAAGAGATATGAGATGATGATGAGTGTGTTGTCGTGCT 2965
Qy      107 ProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValLeuTrpAsnAla 126
Db      2966 GCTATGATGCGAAGATATATGCTG--CCAGCAAAATAAATCTTTTGTGTAATACA 3022
Qy      127 GlnSer---TyrIleLeuTyArgCysGlySerValLysAspGlySerLeuAla----- 143
Db      3023 GACTCAGCTTCAAAAGGCGCTGATTC-----AGAGACATTTAAAGTTGGGTT 3070
Qy      144 ---AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp 162
Db      3071 CANGGTGATGTTTCTCCGATGATCATCATTTTTCACATCTTCTGATGACACAGACA 3130
Qy      163 LeuThrValTrpAspAspLysMetArgCysLeuHisSer----- 175
Db      3131 ATCAGCGCTCGGAGACAAAGAAAGTATGTAAGACTCTGCTGATTAAGACCAAGA 3190
Qy      175 ----- 175
Db      3191 GTAGATGTTGTTTCAAGAAATGAAGATGATGCTCTTCACATTCACATATTAAGACGT 3250
Qy      176 -----GluLysAlaHisAspLeuGlyIleThr 184
Db      3251 CTGCAACTCATTAATGAGAAACAGGTCAATTCATTAATCTGACTGAAGCTCAAGTTAGC 3310
Qy      185 CysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPheArg 204
Db      3311 TGCTGTGCTTAAGTCCACAT-----CTTCACTAC----- 3340
Qy      205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleThrIleValSerPheThrHisIle 224
Db      3341 ATTGATTTTGGAGATGAAATGAGAGCATGAGATTTTAGAATCTGTAACATATAGATC 3400
Qy      225 LeuAlaArgArgThrGluHisGlnLeuLys-----GlnPheThrGluAspTrp 240
Db      3401 TTCAGTCCAGGTTTTCAGCAACAGAAACCTGATGACATTCAGTTCACAGCCGAT-- 3457
Qy      241 SerGluGluValValSerThrTrpLeuCysAlaGlnAsp-LeuLysAspLeuValGlyI1 260
Db      3458 GAGAAAGACTCTTATTTCAGT-----TCTGATATGCTGAAATTCAGGTATGGAAT 3508
Qy      260 ePheLysMetAsnAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGluSerLeuAl 280
Db      3509 TGGCAATTGACAAATGATCTTTCTACAGCCATCAGAAACAGTGAAGACTTTA-- 3566

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Oy      280  aaSphaepleuylsieguserleuGlyLeu-----ArgSerly 293
Db      3567  -GACTCTTGAATAAATTCAGACTGCTTCTTGCTCATTTGATGGAACAGTAGATATGC 3625
Oy      293  gvalleunargylsiegugluLeuArgThrIyValylSerleuser----- 309
Db      3626  AATATTA-----TTACTGGAATAAAGAAAAGCTTGCTGTCGACCAAGTAGACTA 3679
Oy      310  -----SerGlyIleProaspGluDheIleCysProIlethArgGI 323
Db      3680  CTTTCTTGACATTTCTCAGGATGCTACCA---AGTTTCATCTACCTGCTGACAG 3736
Oy      323  uLeuMetIysAspProValIleAlaSer 332
Db      3737  ACTGCAAGATCTGGAGTTTGATCTCC 3764

RESULT 8
US-09-098-310-1
; Sequence 1, Application US/09098310
; Patent No. 6403765
; GENERAL INFORMATION:
; APPLICANT: Alincmti, Emad S.
; TITLE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 480140.438
; CURRENT APPLICATION NUMBER: US/09/098,310
; CURRENT FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7042
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (578)...(4159)
US-09-098-310-1

Alignment Scores:
Pred. No.: 6.65e-16 Length: 7042
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
Gaps: 19

US-10-077-111-13 (1-384) x US-09-098-310-1 (1-7042)
Oy      3  lvsleuIleHstHrLeuAlaAspHISglYAspArValaIaCysCySAlaPheSerPhe 22
Db      2612  GAACTAGAGACACCACTATGATGAGACACTCAGACGAAGCAATGCTGCGCATTTACCAAC 2671
Oy      23  Ser-----LeuLeuAlaThrCysSerleuAspIySthIleArgleuTySer 38
Db      2672  AGTAGTCATCATCTTCTCTTAGCCCTGGCTCAAGTGACGCTGCTTCCAAATTTGGGAT 2731
Oy      39  LeuArgAspHrIethGluLeuProHisSerProleuysPheHstHrTyAlaValHis 58
Db      2732  TTGAATCAA-----AAAGAAATGTCGAAATACCATGTTTGCTCATACAAATTCAGTCAT 2785
Oy      59  CysCySPhosSerProSerGlyHisIleLeuAlaSerCysSerThAspGlyThrThr 78
Db      2786  CACTGCAAGATTTTCCACGAGATGATTAAGCTTTTGCGCTAATTGTTCCAGCTGATGAACCTTA 2845
Oy      79  ValIeuTTPAsenThrGluAsnGly-----GlnMetIeu 89
Db      2846  AAGCTTTGGATGGACCATACGCAAAATGAGAGAAAGCATTAAATGTGAACAGTTCTTC 2905
Oy      90  AlaValMetGluGlnProSerCylSerPro-----ValArgValCysGlnPheSer 106
Db      2906  CTAATTTGGAGACCTCTCAAGAGATATGGAAGTAGATGAAGTGTGTTGCTGCTGCT 2965

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Oy 107 ProhserThrCysLeuAlaSecGlyValAlaIleAspGlyThrValValLeuThrPheAla 126
Db 2366 GCTATAGTGCACAGATATATGCTG--GCAGCAAAAAATATAAATCTTTGTGTGAATATCA 30222
Oy 127 GlnSer---TyrIleuLeuTyrArgCysGlySerValIlysAspGlySerLeuAla----- 143
Db 3023 GACTCAGCTTCAAAAGCGCGCTGATTC-----AGAGCAACATTTAAGTTGGGCTT 30707
Oy 144 ---AlaCysAlaPheSerProAsnGlySerPheIleValThrGlySerSerCynGlyAsp 162
Db 3071 CATGGTGTGATGTTCTTCTCGATGATCATCATTTTGTACATCTTCTGATGACCAACA 3130
Oy 163 LeuThrValTTPAspAspIysMetArgCysLeuHisSer----- 175
Db 3131 ATCAGGCTCTGGAGACAAAGAAAGTATGTAAAGAACTGCTGTATATGTAAACAAAGA 3190
Oy 175 ----- 175
Db 3191 GTACATGTTGTTGTTCAAGAAATGAAGTATGCTCTTGACATGACATATAGAAGCT 3250
Oy 176 -----GlnIysAlaHisAspLeuGlyIleThr 184
Db 3251 CTGCACATCATTAATGGAAGAACAGTCAGATTTGATATGCTGACTGAAGCTCAAGTTAGC 3310
Oy 185 CysCysAspPheSerSerGlnProValSerAspGlyLeuGlnGlyLeuGlnPheArg 204
Db 3311 TGCCTGTTGCTTAACTCCACAT-----CTTCAGTAC----- 3340
Oy 205 LeuAlaSerCysGlyGlnAspCysGlnValIysIleThrIleValSerPheThrHisGle 224
Db 3341 ATTGCATTTGGAGATGAATAATGAGCCATTGACATTTTACAACTTTGAACATAGAAATC 3400
Oy 225 LeuAlaArgArgThrGlnHisGlnLeuLys-----GlnPheThrGlnAspTrp 240
Db 3401 TTCAGATCCAGAGCTTTCACAGCAAGAAACGTATAGCAGATCCAGTCCAGCCGAT--- 3457
Oy 241 SerGlnGlnValIleSerThrTrpLeuCysAlaIleAsp-LeuLysAspLeuValIleGlyI 260
Db 3458 GAGAAAGCTCTTAATTTCAGAT-----TCTGATATGCTGAAATTCAGGTATGGAAT 3508
Oy 260 PheLysMetAsnAsnIleAspGlyLysGlnLeuLeuAsnLeuThrIysGlnSerLeuAl 280
Db 3509 TGGCAATTTGCACAAATGATATTTCTACAGAGCCATCAGAAACAGTGAAGACTTAA-- 3566
Oy 280 AlaAspLeuLysIleGlnSerLeuGlyLeu-----ArgSerLys 293
Db 3567 -GACTCTTGAATAAATTCAGAGCTGCTCTTTCGTGCATTTGATGACAGACAGTGAAGTATGC 3625
Oy 293 sValLeuArgLysIleGlnLeuLeuArgThrLysValIysSerLeuSer----- 309
Db 3626 AATATTAA-----TTACTGGAAATTAAGAAAGAAAGACTTGTCTGTCTCAAGGGTACATA 3679
Oy 310 -----SerGlyIleProAspGlnPheIleCysProIleThrArgGly 323
Db 3680 CTTTCTTGTCACATTTCTCAGATGATCAACA---AGTTTCATCTACCTCTGCTGACAG 3736
Oy 323 uLeuMetLysAspProValIleAlaSer 332
Db 3737 ACTGCAAGATCTGAGATTTTGAATCTCC 3764

RESULT 9
US-09-690-364-21
/ Sequence 21, Application US/09690364
/ Patent No. 6468795
/ GENERAL INFORMATION:
/ APPLICANT: Hong Zhang
/ APPLICANT: Andrew T. Walt
/ TITLE OF INVENTION: ANTISENSE MODULATION OF APAF-1 EXPRESSION
/ FILE REFERENCE: RTS-0190
/ CURRENT APPLICATION NUMBER: US/09/690,364
/ CURRENT FILING DATE: 2000-10-17
/ NUMBER OF SEQ ID NOS: 100
/ SEQ ID NO 21

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; LENGTH: 7042
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (578) ... (4162)
; US-09-690-364-21
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Alignment Scores:	
Pred. No.:	6,65e-16
Score:	227.00
Percent Similarity:	40.2%
Best Local Similarity:	22.88%
Query Match:	11.09%
DB:	3
Gaps:	19
Length:	7042
Matches:	102
Conservative:	63
Mismatches:	140
Indels:	105

US-10-077-111-13 (1-384) x US-09-690-364-21 (1-7042)

Qy	3	lyleuullenhstlrleuallaaasphiglyasprapvalancyscysalaphesrpe	22
Db	2612	gaaactagatgacacstttagatgacactcmagcaagtaactatgtctgcatttaccacac	2671
Qy	23	ser-----leuleuallathrcysserleuaspylstrllaearyltyrser	38
Db	2672	agtagtcatacatcttctcttagccactggtgcamaagtaactgtcttcctcaaacctttggag	2731
Qy	39	leuargasphehtrguleuprohisserproleuylsprehstlrtyralavalhis	58
Db	2732	ttgmatca-----aaagatgtcgaaatgccatgttggtcattacamaatttcagtcatt	2785
Qy	59	cyscyscyspbeserproserglyhislleuallasercyssestrhnapgltyrthr	78
Db	2786	cactgcagatttttaccacagatgataagcttttgctagtgttctacgctgataaccta	2845
Qy	79	valleutrpasnthrgluasnily-----glmetleu	89
Db	2846	aagctttggatggcagcatcgcaaatgacgaaagaaacattatgtgaaacattcttc	2905
Qy	90	alavalmetgluglnproserglyserpro-----valargvalcysglnpbeser	106
Db	2906	ctaaattttggagacccttcacagacagatagagactgataaggaagtggtgttcctgcgt	2965
Qy	107	proaspserthrhcysleuallaserglyalalaaaspglythrvalleutrpasna	126
Db	2966	gcgtatgctgcagagatataagtcg-----gcagcaaaaaataaactcttttggaatata	3022
Qy	127	glnser--tyrlyleutryrargcysglyservallysaspglyserleuala-----	143
Db	3023	gactcacggttcaaaagtggtcgattgc-----acagacacatttaagttgaggt	3070
Qy	144	---alacysalapheserproasnilyserphehevalthrglysercscysglyasp	162
Db	3071	cangctgtagattgtttctcctgtagatgacatcatttttgacactcttgatgaccagaca	3130
Qy	163	leuthrvaltrpaspaplysmetargcysleuhisser-----	175
Db	3131	atcagcgtctgcgacacaaamaagatgtaagaactctgctgtaactttaaacacaga	3190
Qy	175	-----	175
Db	3191	gtagatgttggtttcaagaaaatgaaatgtagtgcttcgcattgacatataagact	3250
Qy	176	-----glnylsalahisapyleuclilthr	184
Db	3251	ctgcactcatttaatgcagacacgctcagattgattatctgactgaaagctcaagttgac	3310
Qy	185	cyscysaspbeserseqinprovalseraspeluglincglyleuainpheharg	204
Db	3311	tgctgttgcttaagtcacat-----cttcagctac-----	3340
Qy	205	leuallasercysglyglnaspcysglnvalylsletrpilevalserphehtrhisile	224
Db	3341	atttcacatttggagatgaaaatgagccatttagatttttagaactttgtaaacatagaatc	3400

```

Oy 225 LeuAlaArgAlGThrGluHisGlnLeuLys-----GlnPheThrGluAspTrp 240
Db 3401 TTCCAGTCCAGGTTTCAGCACAGAGAAACTGTATGGCACATCCAGTTCCACGCCAT--- 3457
Oy 241 SerGluGluValAlaSerThrTyrPheCysAlaGlnAsp-LeuLysAspLeuValGlyI 260
Db 3458 GAGAAAGACTCTTATTTCAAGT-----TCTGATGATGCTGAAATTAGGATAGAAAT 3508
Oy 260 ePheLysMetAsnAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGluSerLeuAl 280
Db 3509 TGGCAATGAGCAATATGATGATCTTTCTACAGAGCCATCAGAAACAGTGAACGTTTA-- 3566
Oy 280 aAspAspLeuLysIleGluSerLeuGlyLeu-----ArgSerLys 293
Db 3567 -GACTCTTGAAAAATTCACAGCTGCTTTCTTGTCATTTGATGAAACACTGAAGGTATGC 3625
Oy 293 sValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeuSer----- 309
Db 3626 AATATTA-----TTACTGCAAAATAAGAAAAGACTTTGTCTGTCCACAGGATACAGTA 3679
Oy 310 -----SerGlyIleProAspGluPheIleCysProIleThrArgG1 323
Db 3680 CTTTCTTGTCACATTTCTCAGGATCTCAACA--AGTTTCATCTACCTCTGCTGACAAG 3736
Oy 323 uLeuMetLysAspProValIleAlaSer 332
Db 3737 ACTGCAGAAATCTGCAGTTTGATCTCC 3764

RESULT 10
US-09-949-016-159
: Sequence 159, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001107
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 159
: LENGTH: 7042
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-159

Alignment Scores:
Pred. No.: 6,656-16 Length: 7042
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: Gaps: 19
US-10-077-111-13 (1-384) x US-09-949-016-159 (1-7042)

Oy 3 LysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysGlyAlaPheSerPhe 22
Db 2612 GAACTAGTACACACCTATGATGAGCACTCAGAGCAAGTCMAATGTCGCCATTTCACACCAAC 2671
Oy 23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSer 38
Db 2672 AGTAGTATCATCTTCTTACCCACCTGGGTCAAGTACTGCTTCTCAAACTTTGGGAT 2731
Oy 39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHis 58

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Db      2732 TTGAATCA-----AAAGATGCGAAATACCATGTTTGGTCAATACAAATTCAGTCAAT 2785
QY      59 CysCysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrArgGlyThr 78
Db      2786 CACTGCAGATTTTCACAGATGATTAACGCTTTGGCTAGTTGTCACGCTGATGGAACTTGA 2845
QY      79 ValLeuThrPenthrgluAangly-----GlnMetLeu 89
Db      2846 AACCTTTGGATGCGACATCAGCAAAATGAGAGAAAACATTAATGCAACGCTTCTTC 2905
QY      90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
Db      2906 CTAATATTGGAGAGCCTCAAGAGATATGAGATGATGAGTGAAGCTGTGTGCTGCTCT 2965
QY      107 ProAlaPseThrCysLeuAlaSerGlyAlaAlaAspGlyThrValValLeuThrPseAla 126
Db      2966 GCTGATGTGTCAGAGATATGCTG--GCAGCAAAAATAAATCTTTTGTGGAAATACA 3022
QY      127 GlnSer---TyrIysLeuTyrArgCysGlySerValIysAspGlySerLeuAla----- 143
Db      3023 GACTCAGCTTCAAAAGCTGCTGATGC-----AGAGACATTTTAAGTTGGCTT 3070
QY      144 --AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp 162
Db      3071 CATGCTGTGATGTTTCTCTCGATGATCATCATTTTGAACATCTTCTGATGACACAGACA 3130
QY      163 LeuThrValThrPseAspIysMetArgCysLeuHisSer----- 175
Db      3131 ATCAGGCTTGAGAGACAAAGAAAGATGTAGAGAACTCTGTATATGTTAAGCAAGAA 3190
QY      175 ----- 175
Db      3191 GTAGATGTTGTCTTCAAGAAATGAAGTATGCTCTTGACATGACCATATPAAGCGT 3250
QY      176 -----GluIysAlaHisAspLeuGlyIleThr 184
Db      3251 CTCGAACTCATTAATGAGAGAACAGCTCAGATTGATTATCTGACTGAAGCTCAAGTTAAGC 3310
QY      185 CysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPhePheArg 204
Db      3311 TGGTGTGCTTAATAGTCCACAT-----CTTCAGTAC----- 3340
QY      205 LeuAlaSerCysGlyGlnAspCysGlnValIysIleThrIleValSerPheThrHisIle 224
Db      3341 ATTCCATTGGAGATGAAATGAGCCATTCAGATTTTGAACCTGTAAACATACGAATC 3400
QY      225 LeuAlaArgIleGthrGluHisGlnLeuIys-----GlnPheThrGluAspTrp 240
Db      3401 TTCACATGCCAGGTTTCAGCACAGAAAACGTATGACATCCAGTTCACAGCCGAT--- 3457
QY      241 SerGluGluValIysThrTrpLeuCysAlaGlnAsp-LeuIysAspLeuValIleGlyI 260
Db      3458 GAGAGACATCTTAATTCACAG-----TCTGATATGCTGAAATTCAGAGTATGGAAT 3508
QY      260 CpeHlyMetAsnAsnIleAspGlyIysGluLeuLeuAsnLeuThrIysGluSerLeuAl 280
Db      3509 TGGCAATTTGCAAAATGATCTTTCTACAGGCCATACAGAAACAGTGAAGACTTTA-- 3566
QY      280 AspAspLeuIysIleGluSerLeuGlyLeu-----ArgSerIly 293
Db      3567 -GACTCTTGAATAATTCAGAGCTGCTTCTTGTCATTTGATGAGACAGTGAAGGTATGG 3625
QY      293 eValLeuArgIlyIleGluGluLeuArgThrIysValIysSerLeuSer----- 309
Db      3626 AATATTTA-----TTACTGGAATAAAGAAAAGACTTTGTCTGTCTCCAGGGGTACAGTA 3679
QY      310 -----SerGlyIleProAspGluPheIleCysProIleThrArgI 323
Db      3680 CTTTCTTGTCACATTTCTCAGAGATCCACCA--AGTTTCATCTACTCTCTGCTGACAG 3736
QY      323 uLeuMetIysAspProValIleAlaSer 332

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Db      3737 ACTGAAAGATCTGAGTTTGTGATCTCC 3764
RESULT 11
US-09-092-508-15
; Sequence 15, Application US/09092508
; Patent No. 6291643
; GENERAL INFORMATION:
; APPLICANT: Henzel, William J.
; TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Wejter & Schmidt
; STREET: 3100 No. 6291643west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,508
; FILING DATE: 05-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,807
; FILING DATE: 05-JUN-1997
; APPLICATION NUMBER: 60/055,258
; FILING DATE: 07-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kertelberger, Ph.D., Denise M
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 11669-6USU1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 578...4192
; OTHER INFORMATION:
US-09-092-508-15
Alignment Scores:
Pred. No.: 6.7e-16 Length: 7075
Score: 227.00 Matches: 102
Percent Similarity: 40.24% Conservative: 63
Best Local Similarity: 24.88% Mismatches: 140
Query Match: 11.09% Indels: 105
DB: 3 Gaps: 19
US-10-077-111-13 (1-384) x US-09-092-508-15 (1-7075)
QY      3 LysLeuIleHisThrLeuAlaAspHisGlyAspArgValAsnCysCysAlaPheSerPhe 22
Db      2645 GAAGTAGTACACACCTATGATGAGCACTCAGACCAAGTCAATTGCTGCCATTTTACCAC 2704
QY      23 Ser-----LeuLeuAlaThrCysSerLeuAspIlyThrIleArgLeuTyrSer 38
Db      2705 AGTAGCATCATCTTCTCTTAGCCACTGGGTCAAGTCAAGTCTGCTCAAACTTTGGGAT 2764
QY      39 LeuArgAspPheThrGluLeuProHisSerProLeuIysPheHisThrTyrAlaValHis 58
Db      2765 TTGAATCA-----AAAGATGTCGAAATACCATGTTTGGTCAATATTCAGTCAAT 2818

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QY 59 CysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThr 78
DB 2819 CACTGCAGATTTCACACAGATGATTAACCTTTGGCTAGTTGTCAGCTGATGCAACTT 2818
QY 79 ValLeuTrpAsnThrGluAsnGly-----GlnMetLeu 89
DB 2879 AAGCTTTGGATGCGATCAGCAAAATGAGAAAAACATTAATGTGAACAGTTCTTC 2938
QY 90 AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer 106
DB 2939 CTAATTGAGAGACCTCAAGAGATATGAGACTGATGAGAGCTGTTGCTGCTCT 2998
QY 107 ProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValLeuTrpAsnAla 126
DB 2999 GCTGATGCTGCAAGATTAATGCTG--GCAACCAAAAATAAATCTTTTGTGGAAATCA 3055
QY 127 GlnSer---TyrLysLeuTyrArgCysGlySerValLysAspGlySerLeuAla----- 143
DB 3056 GACTCAGCTTCAAAAGTGGCTGATTC-----AGAGACATTTTAAGTTGGGTT 3103
QY 144 ---AlaCysAlaPheSerProAsnGlySerPheValThrGlySerSerCysGlyAsp 162
DB 3104 CATGCTGTGATGTTTCTCTGATGATCATCATTTTGAATCTCTGATGATGACACAGA 3163
QY 163 LeuThrValTrpAspAspLysMetArgCysLeuHisSer----- 175
DB 3164 ATCAGCTCTGGGACAAAGAAAGTATGTAGAACTCTGCTGTAATGTAAACCAAGAA 3223
QY 175 ----- 175
DB 3224 GTAGATTTGTGTTTCAAGAAATGAAGTATGCTCTTGACATTTGACATTAAGACT 3283
QY 176 -----GluLysAlaHisAspLeuGlyIleThr 184
DB 3284 CTGCACACTCATTAATGAGAAACAGCTCAGATTGATTATCTGACTGAAGCTCAAGTTAGC 3343
QY 185 CysCysAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPhePheArg 204
DB 3344 TGCTGTGCTTAATGCTCAGAT-----CTTCAGTAC----- 3373
QY 205 LeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSerPheThrHisIle 224
DB 3374 ATTGCATTTGGAGATGAATAATGAGCCATTGAGATTTTAAGAACTGTAAACAATAGATC 3433
QY 225 LeuAlaArgArgThrGluHisGlnLeuLys-----GlnPheThrGluAspTrp 240
DB 3434 TTCCAGTCCAGGTTTCAGCACAAACAACTGATGACATCCAGTTCACAGCCGAT-- 3490
QY 241 SerGluGluValValSerThrTrpLeuCysAlaGlnAsp---LeuLysAspLeuValGlyI 260
DB 3491 GAGAGACCTCTTAATTCAAGT-----TCTGATATGCTGAATAATTCAGATGAGAT 3541
QY 260 ePheLysMetAsnAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGluSerLeuAl 280
DB 3542 TGGCAATTGGCAAAATGATATCTTTCTAGAGCCATCAGAAACAGTGAAGACTTTA-- 3599
QY 280 AspAspLeuLysIleGluSerLeuGlyLeu-----ArgSerLys 293
DB 3600 -GACTCTTGAATAAATTCAGACAGCTCTTGTGTCATTTGATGAGACAGTGAAGGTATGC 3658
QY 293 eValLeuArgLysIleGluGluLeuArgThrLysValLysSerLeuSer----- 309
DB 3659 AATATTA-----TTACTGGAAATTAAGAAAAAGACTTTGTCTCTCAACAGGGTACAGTA 3712
QY 310 -----SerGlyIleProAspGluPheIleCysProIleThrArgI 323
DB 3713 CTTTCTTGATGACATTTCTCAGGATGATACCA---AGTTTTCATCTACTCTGCTGACAG 3769
QY 323 uLeuMetLysAspProValIleAlaSer 332
DB 3770 ACTGCAAAAGATCTGAGTTTGTATCTCC 3797
```

```
RESULT 12
US-09-435-115-15
: Sequence 15: Application US/09435115
: Patent No. 6346607
: GENERAL INFORMATION:
: APPLICANT: Henzel, William J.
: TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF CASPASE-3
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
: STREET: 3100 No. 634607west Center, 90 South Seventh St
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/435,115
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/092,508
: FILING DATE:
: APPLICATION NUMBER: 60/055,258
: FILING DATE: 07-AUG-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Kettelberger, Ph.D., Denise M
: REGISTRATION NUMBER: 33,924
: REFERENCE/DOCKET NUMBER: 11669.6USU1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-332-5300
: TELEFAX: 612-332-9081
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7075 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 578...4192
: OTHER INFORMATION:
: US-09-435-115-15
: Alignment Scores:
: Pred. No.: 6,7e-16 Length: 7075
: Score: 227.00 Matches: 102
: Percent Similarity: 40.24% Conservative: 63
: Best local Similarity: 24.88% Mismatches: 140
: Query Match: 11.09% Indels: 105
: Gaps: 19
US-10-077-111-13 (1-384) x US-09-435-115-15 (1-7075)
QY 3 LysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPheSerPhe 22
DB 2645 GAATTAAGTACCACTTATGATGACCACTCAGAGCAAGTCAATTCCTCCATTCCACCAAC 2704
QY 23 Ser-----LeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSer 38
DB 2705 AGTAGATCATCATCTTCTTAGCCACTGGGTCAGAGTACGCTTCCCAAACTTGGGAT 2764
QY 39 LeuArgAspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHis 58
DB 2765 TTGAATCAA-----AAAGATGTGAAATAACCATGTTGGCTATACAAATTCAGTCAAT 2818
QY 59 CysCysPheSerProSerGlyHisIleLeuAlaSerCysSerThrAspGlyThr 78
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Db	2819	CACCTGCAGATTTTCCACGACGATGATAAGCTTTGGCTTAATTGTTTCAAGCTGATGCAACTTA	2878
Oy	79	ValLeuTrpAenThrGluAsnGly-----GlnMetLeu	89
Db	2879	AAGCTTTGGGATGCGACATCCAGCAAAATGAGAGAAACATTAAATGTGMAACAGTTCTTC	2938
Oy	90	AlaValMetGluGlnProSerGlySerPro-----ValArgValCysGlnPheSer	106
Db	2939	CTAAATTGGAGAGACCTTCMAAGAGATATGGAAGTATAGATGATGATGTTGTTGCTGGCTG	2998
Oy	107	ProApsSerThrCysLeuAlaSerGlyValAlaAspGlyThrValValLeuTrpAsnAla	126
Db	2999	GCTGATGTGTCMAAGGATATGATGTTG--GCAGCAAAAAATTAATCTTTTGTGGAAATCA	3055
Oy	127	GlnSer---TyrLysLeuTyrArgCysGlySerValLysAspGlySerLeuAla-----	143
Db	3056	GACTCAGCTTCAAAAGGTGGCTGATTTGC-----AGAGCACAATTAAAGTTGGGTT	3103
Oy	144	--AlaCysAlaPheSerProAsnGlySerPhePheValThrGlySerSerCysGlyAsp	162
Db	3104	CATGGTGTGATGTTTCTTCCTGATGATCAATCATTTTGGACATCTTCGTGATGACCAGACA	3163
Oy	163	LeuThrValTTPAspAspLysMetArgCysIleuHisSer-----	175
Db	3164	ATCAGGCTCTGGAGACAAAGAACTAGTAAGAACTCTGCTGTAATGTTAAAGCAAGAA	3223
Oy	175	-----	175
Db	3224	GTAAGTGTGTTGTTTCCAAAGAAATGAAGTGAATGCTCTTCGACATTTGACCATATAAGAGCT	3283
Oy	176	-----GluValAlaHisAspLeuGlyTLeThr	184
Db	3284	CTGCAACTCATTAATGAGAAGAAACAGATCAGATTGATTTATCTGACGAAAGCTCAAGTTAGC	3343
Oy	185	CysCysAspPheSerSerGlnProAlaSerAspGlyGlnGlnGlyLeuGlnPhePheArg	204
Db	3344	TGCTGTGCTTAAAGCCACAT-----CTTCAGATAC-----	3373
Oy	205	LeuAlaSerCysGlyGlnAspCysGlnValLysIleTrpIleValSerPheThrHisIle	224
Db	3374	ATTGATTTGGAGATGAATAATGAGCCATTTGAGATTTTAAAGAACTGTAAACATATGAAATC	3433
Oy	225	LeuAlaArgTrpGlnHisGlnLeuLys-----GlnPheThrGlnAspTrp	240
Db	3434	TTCCAGTCCAGAGTTTCCACACAAAGAAACGTATGACATCCAGTTCCAGCCGAT---	3490
Oy	241	SerGlnGluValAlaIleSerThrTyrLeuCysAlaGlnAsp-LeuLysAspLeuValGlyIle	260
Db	3491	GAGAAAGACTCTTATTTCAAGT-----TCTGATGTCGTGAATTCAGAGTATGAAAT	3541
Oy	260	ePheLysMetAsnAsnIleAspGlyLysGlnLeuLeuAsnLeuThrLysGlnSerLeuAl	280
Db	3542	TGGCAATTGACCAATATGATCTTTTCTACGAGGCCATCCAGAAACAGTGAAGACTTAA-	3599
Oy	280	AspAspLeuLysIleGlnSerLeuGlyLeu-----ArgSerLys	293
Db	3600	-GACTCTTGAATAAATTCAGAGACTGCTTCTTGTCATTTGATGGAACAGTGAAGATATGG	3658
Oy	293	sValLeuArgLysIleGlnGluLeuArgThrLysValLysSerLeuSer-----	309
Db	3659	AATATTA-----TTACTGGAATAATTAAGAAAAAGCTTTGTCTGTCAACAGAGTAAAGTA	3712
Oy	310	-----SerGlyIleProAspGlnPheIleCysProIleThrArgIle	323
Db	3713	CTTCTCTTGACATTCTTCAGCAGTCTTACA--AGTTTCATCTTACCTGTGTGACAAAG	3769
Oy	323	uLeuMetLysAspProValIleAlaSer	332
Db	3770	ACTGCAAAGACTCTGGAGTTTGTGATGCTTC	3797

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; Sequence 145 Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhimei
; APPLICANT: John Thilghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662ol Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_files Version 1.0
; SEQ ID NO 145
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (184)..(1236)
; US-09-620-312D-145

Alignment Scores:
Pred. No.: 9,6e-17 Length: 2130
Score: 226.50 Matches: 96
Percent Similarity: 41.058 Conservative: 60
Best Local Similarity: 25.268 Mismatches: 137
Query Match: 11,064 Indels: 88
DB: 4 Gaps: 15

US-10-077-111-13 (1-384) x US-09-620-312D-145 (1-2130)
QY 25 LeuAlaTThCySerLeuAlaSprLySThrIleArgLeuTySeriLeuAlaGlnPhnThGlu 44
D 149 CTAGCTACAGCTTCCTCGAAGACAAATCCATAATAGATGAGAGCATG-----TATCGCCAG 202
QY 45 LeuPronHisSerProLeuLysPheLeuHisThrTyAlaValAlaHisCysCysCysPheSerPro 64
D 203 CGCTTCCTGTATTCCTTGATGATGACATACACACTGTGTACCGCTGTGCCA-ATTGTACC 261
QY 65 SerGlyHisIleLeuAlaSerCysSerThrAspGlyThrValLeuThrValLeuTrpAsnThrGlu 84
D 262 GATGGAAGACATAATTGTGTGTCATGTAGTGAAGATAAACTTATTAATAATTTGGATACACACA 321
QY 85 AsnGlyGlnMetLeuAlaValAlaMetCysLysIleProSerGlySerProValaGuaCysGln 104
D 322 AATAACCAATGCTTAAATACCTTCTCAGATTCCGTTGATTT--GCAATTTTGTGGAC 378
QY 105 PheSerProAspSerThrCysLeuAlaSerGlyAlaAlaAspGlyThrValValLeuTrp 124
D 379 TTTAACCTTAAGTGTATCATGATCATACCTTACAGAGGTTGTGTATCAAACTGTGAAGTCTGG 438
QY 125 AsnAlaGlnSerTyLysLeuTyArgCysGluSerValaLysAspGlySerLeuAlaAla 144
D 439 GATGTAAAGGTGAACAAATTTACTACAGATTACCAAGTTACACAGCGGTGAGTTAATTGC 498

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Qy	145	ysalalapheserProAsnGlyserPheValThrnglySerSerCysgluAspLeuThr	164
Db	499	ATATCATTCATCTTGGGTACTATCTCATCAACAGCTTCTTCAGATGATACCTTAAG	558
Qy	165	ValTrpAsp---AspIysMetArgCysLeuHisSerGluValalaHisAspLeuGlyLe	183
Db	559	ATTCTGCAGCTCTTGAAGGAAGGCGCATCTTATACCTTCAAGACATACGGGACCTGTC	618
Qy	184	ThrCysCAspPheSerSerGlnProValSerAspGlyGluGlnGlyLeuGlnPhePhe	203
Db	619	TTTACTGCTTTCATTTTCA-----AAAGCTGAGAGCTATTAT	654
Qy	204	ArgLeuAlaSerCysGlyGlnAspCysGlnValIysIleTrpIleValSerPheThrHis	223
Db	655	-----GCATCGAGAGGTCACACACACAGGCTTATTATGAGACATACTTTGATGAA	708
Qy	224	IleLeuAlaArg---ArgThrGlnHisGlnLeuIysGlnPhe-----	236
Db	709	TTGCATGTGTAAGGCTTACCAAAAGAAATCTCAAAAGATTCATTTGATTGATTCACCACA	768
Qy	237	-----ThrGluAspTrpSerGluGluValValSerThrTrp	248
Db	769	CATCTTCTGTATATCTACCCAGAACACACACATCCCATGAGAGAAAAGTTGAGACT---	825
Qy	249	LeuCysAlaGlnAspLeuIysAspLeuValGlyIlePhe---LysMetAsnAlaIleAsp	267
Db	826	-----GTAGAAATTAATCCAAAGCTTGAGGTATATCAT	858
Qy	268	GlyIysGlnLeuLeuAsnLeuThrIysGlnSerLeuAlaAspAspLeuIysIleGlnSer	287
Db	859	-----TTCCAGATCTCTACTCCCTCGTTATGAGATATCTTCTTTGATTCT	906
Qy	288	LeuGlyLeuArgSerLeIysValLeuArgIysIleGluGlnLeuArgThrIysValIysSer	307
Db	907	-----ACCACCAACAAACGAAACC	924
Qy	308	LeuSerSerGlyIleProAspGlu-----PheIleCysProIle	320
Db	925	AGTGTAGACTCTCTCCACACAAAGGTGAAGAGCCTGTGATATTTCTTGAACCT---	981
Qy	321	ThrArgIleuMetLeuIysAspProValIleAlaSerAspGlyTyrSerTyrGluIysGln	340
Db	982	-----TCCTTATATGTCACCAAGATGTTGGCAACA-----	1011
Qy	341	AlaMetGluAsnTrpIleSerIysIysIysArgThrSerProMetThrAsnLeuValLeu	360
Db	1012	-----ACCACGAAAAAGAAACGAAAGACATGATGATCCTCCCTGT	1053
Qy	361	ProSerAlaValIleuThrProAsnArgThrLeuIysMetAlaIleAsnArgTrpLeuGln	380
Db	1054	GAAGT-----CAAGAGACATACCTCTGCTGTGACTGATGCTTTAGAG	1098
RESULT 14			
DS-10-101-464A-251			
Sequence 251, Application US/10101464A			
Patent No. 6768041			
GENERAL INFORMATION:			
APPLICANT: Strabala, Timothy			
APPLICANT: Nieuwenhuizen, Nicolaas			
APPLICANT: Higgins, Colleen M.			
TITLE OF INVENTION: Compositions Isolated from Plant Cells			
FILE REFERENCE: 11000.1020C2			
CURRENT APPLICATION NUMBER: US/10/101,464A			
CURRENT FILING DATE: 2002-03-18			
PRIOR APPLICATION NUMBER: 09/704,302			
PRIOR FILING DATE: 2000-11-01			
PRIOR APPLICATION NUMBER: 09/228,986			
PRIOR FILING DATE: 1999-01-12			
PRIOR APPLICATION NUMBER: 60/162,866			
PRIOR FILING DATE: 1999-11-01			
PRIOR APPLICATION NUMBER: PCT/US00/00724			

PRIOR FILING DATE: 2000-01-11			
NUMBER OF SEQ. ID NOS: 989			
SOFTWARE: FASTSEQ for Windows Version 4.0			
SEQ ID NO 251			
LENGTH: 937			
TYPE: DNA			
ORGANISM: Eucalyptus grandis			
US-10-101-464A-251			
Alignment Scores:			
Pred. No.: 1,24e-16 Length: 937			
Score: 220.50 Matches: 80			
Percent Similarity: 34.15% Conservative: 32			
Best Local Similarity: 24.39% Mismatches: 87			
Query Match: 10.77% Indels: 129			
DB: 4 Gaps: 12			
US-10-077-111-13 (1-384) x US-10-101-464A-251 (1-937)			
QY	135	GIYSerValIySaSPoLYSeRLeuAlaIaCYsAlaPheSeRProAsnGIYSeR-----	152
Db	74	GGTTCAATGCCCAAGAAATCCTGGTCTCTGTGNTAGTACACTCCCTTAATGGAAGTCCAA	133
QY	153	-----PhePheValThrGIYSeRSeRcYSeGIYsPLeuThrValITTPaSPaSPLeuMet	170
Db	134	GATTACCTTTTCCGGAAAGGCAACAGTTCCTCC-----TTATTATGGAGATGCTGAATT	187
QY	171	Arg-----Cys-----LeuHisSeRGIYsAlaHis---	177
Db	188	CGAATATTGCTGAGATCTCGACTGCTGCTTGTCTTGTTCCTTGAACCTGGAAG	247
QY	180	-----AsPLeuGIYIleThr	184
Db	248	ATTGTTCAAGGTGATCTGAACCTGAGAATGTCCTTGTATCTGATCTTACCTGCAAG	307
QY	185	CYSCySaSPheSeR-----	189
Db	308	ATATGATTTTGGGATTTCTAGCGTTGTAGTGAGCACTCTTCCTGCCCAAGTTTC	367
QY	190	-----SerGIYProValSeRAsPLeuGIYGIYLeuGIYLeuGIY	201
Db	368	CGCGCATCAACAGAGCCAAAGCGTCTTTCTTATACAGATTCAGAG-----	415
QY	202	PhePheArgLeuAlaSeRcYSeGIYsAlaSPcYSeGIYValIYsIleTPRIleValSeRPhE	221
Db	416	TTCTACAGGAGATGAAGAACTTGAAGCCCAATCTGATGTTTCTTGTGTGTCGATCATC	475
QY	222	ThrHisIleLeu-----	225
Db	476	CTACATTTACTCACTGCTGTAACCACTTACCTGGTTAGTCCCTGAGGTGATTAAGCAAA	535
QY	226	---AlaArgArgThrGIYHisGIYLeuYSeGIYnPhethrGIYAsPTrSPSeRGIYVal	244
Db	536	TCATCCAAATAATTGAGAGTCGGTTTGGATCAATCAGCTGACAAATGAGCCCTGCTGTGA	595
QY	245	ValSeRThrTrPLeuCYsAlaGIYnSPLeuYsAsPLeuValGIYIlePheIYsMetAsn	264
Db	596	GCA-----	598
QY	265	AsnIleAsPGLYSeGIYLeuDeuAlaSnLeuThrIYSeGIYSeRLeuAlaAsPAsPLeuLYs	284
Db	599	-----CTCGA	604
QY	285	IleGIYSeRLeuGIYLeu-----ArgSeRVal---	294
Db	605	TTAGTGAACCTGGCTTTCATATGCTGTATTTTAAACGGTGAAGATGACCCCAATAATTACA	664
QY	295	-----LeuArgTrYsIleGIYLeuYnArgTrYrYsValIYSeRSeRLeuSeRSeRGIY	311
Db	665	CTGCGCTTTGTAGGAATTTGAGACAGCTGCTAC-----TCTGAAGAGCCAGCG	715
QY	312	IlePTrAsPGLuPheIleCYsProIleThrArgGIYLeuMetLYsAsPProValIleAla	331

